

SEARCH REQUEST FORM

Requestor's Name: Sally Teng Serial Number: 08/426,509
Date: 1/27/97 Phone: 308-4230 Art Unit: 1812

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

- Please search
- ① amino acids ^{SH₃} 48 to 111, ^{Kinase} 233-478, ^{SH₂} + 122-196
of SEQ ID NO: 2
- ② amino acids ^{SH₂} 25 to 109, ^{SH₃} 296-375, ^{SH₃} + 192-234,
^{Kinase} + 424 to 659 of SEQ ID NO: 4
- ③ amino acids 122 to 201, ^{SH₂} 54 to 112, ^{SH₃} + 247 to 426,
of SEQ ID NO: 6
- ④ amino acids 493-507 of SEQ ID NO: 2
- ⑤ amino acids 666-675 of SEQ ID NO: 4

STAFF USE ONLY

1-552

Date completed: <u>02-04-97</u>	Search Site	Vendors
Searcher: <u>Beverly W. G. G. G.</u>	<input type="checkbox"/> STIC	<input type="checkbox"/> IG
Terminal time: <u>15</u>	<input type="checkbox"/> CM-1	<input type="checkbox"/> STN
Elapsed time: _____	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: <u>27</u>	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: <u>1</u>	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>WIP</u>

Title: >US-08-426-509-4
Description: (192-234) from US08426509.pep (3 of 5)
Perfect Score: 290
Sequence: 1 AQYDNESKKNYGSQPPSSSTSLAQYDSNSKKIYGSQPNFNMQY 43

Scoring table: PAM 150
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 31.496; Variance 62.651; scale 0.503

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query	Match	Length	DB	ID	Description	Pred. No.
1	80	27.6	473	14	S61428	late embryogenesis a	3.31e-01		
2	77	26.6	458	9	S33520	Lea protein - soybea	8.66e-01		
3	77	26.6	655	5	A55726	RNA-binding protein	8.66e-01		
4	77	26.6	656	5	A49358	RNA-binding protein	8.66e-01		
5	76	26.2	2710	8	A37052	toxin A - Clostridiu	1.19e+00		
6	76	26.2	2710	8	S08638	toxin A - Clostridiu	1.19e+00		
7	74	25.5	870	8	S27514	mosquitocidal toxin	2.22e+00		
8	72	24.8	462	13	S33798	FUS-CHOP mutant fusi	4.11e+00		
9	72	24.8	526	5	S33799	RNA-binding protein	4.11e+00		
10	70	24.1	286	9	S32480	hypothetical protein	7.52e+00		
11	70	24.1	1538	3	RGBYS3	regulatory protein S	7.52e+00		
12	70	24.1	1986	10	S28353	probable polyketide	7.52e+00		
13	69	23.8	173	8	S38231	hypothetical protein	1.01e+01		
14	69	23.8	774	3	QRECFA	iron(III) dicitrate	1.01e+01		
15	68	23.4	213	4	S26055	2-dehydro-3-deoxypho	1.36e+01		
16	68	23.4	328	4	S16300	UDPglucose 4-epinera	1.36e+01		
17	68	23.4	396	10	S58223	LSR1 protein - yeast	1.36e+01		
18	68	23.4	396	10	S61136	probable transcripti	1.36e+01		
19	68	23.4	573	12	S20710	hypothetical protein	1.36e+01		
20	68	23.4	1394	10	A29637	position-specific an	1.36e+01		
21	67	23.1	231	8	F64120	phosphate regulon tr	1.83e+01		
22	67	23.1	316	9	S58719	hypothetical protein	1.83e+01		
23	67	23.1	439	9	A36911	glutamine synthetase	1.83e+01		
24	67	23.1	664	10	S53037	PLB1 protein - yeast	1.83e+01		
25	67	23.1	889	10	S50934	hypothetical protein	1.83e+01		
26	67	23.1	1196	14	S35994	XP-G-related protein	1.83e+01		
27	66	22.8	288	6	I36848	ABR protein - variol	2.44e+01		
28	66	22.8	320	10	S09208	chorion protein s36	2.44e+01		
29	66	22.8	433	2	ITHUC	alpha-1-antichymotry	2.44e+01		
30	66	22.8	505	10	S44647	f42h10.1 protein - C	2.44e+01		
31	66	22.8	930	10	D37271	A-alpha 7 4 protein	2.44e+01		
32	66	22.8	1094	9	S49313	protein kinase - sli	2.44e+01		
33	66	22.8	1094	9	S52076	protein kinase - sli	2.44e+01		
34	66	22.8	1146	10	S46837	hypothetical protein	2.44e+01		
35	65	22.4	107	4	B60754	glucan 1,4-alpha-glu	3.25e+01		
36	65	22.4	131	7	JC1369	hypothetical 14.2K p	3.25e+01		

37	65	22.4	270	8	H64248	hypothetical protein	3.25e+01
38	65	22.4	657	4	A64079	2',3'-cyclic-nucleot	3.25e+01
39	65	22.4	1468	12	A44345	nucleoporin - rat	3.25e+01
40	64	22.1	125	10	S53086	ND3 protein - jelly	4.32e+01
41	64	22.1	295	13	S36174	RNA binding protein/	4.32e+01
42	64	22.1	330	14	J02262	Polygalacturonase in	4.32e+01
43	64	22.1	397	1	XNECY	tyrosine transaminas	4.32e+01
44	64	22.1	459	6	J02345	major capsid protein	4.32e+01
45	64	22.1	877	9	S58824	hypothetical protein	4.32e+01

ALIGNMENTS

RESULT 1

ENTRY S61428 #type complete
 TITLE late embryogenesis abundant protein (clone pGPM10) - soybean
 ORGANISM #formal_name Glycine max #common_name soybean
 DATE 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 01-Mar-1996
 ACCESSIONS S61428
 REFERENCE S61428
 #authors Chow, T.; Hsing, Y.C.; Chen, Z.
 #submission submitted to the EMBL Data Library, October 1993
 #description cDNA sequences for a soybean seed maturation polypeptide gene family.
 #accession S61428
 ##status preliminary
 ##residues 1-473 ##label CHO
 ##cross-references EMBL:U02966
 SUMMARY #length 473 #molecular-weight 50982 #checksum 278

Query Match 27.6%; Score 80; DB 14; Length 473;
 Best Local Similarity 21.6%; Pred. No. 3.31e-01;
 Matches 8; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Db 195 dyatqktkdyasdatdaakktkdyaqktkdyaseas 231
 :| : |:|:|: : :| : | |:|:|:
 Qy 193 QYDNESKKNYGSQPPSSSTSLAQYDSNSKKIYGSQPN 229

RESULT 2

ENTRY S33520 #type complete
 TITLE Lea protein - soybean
 ORGANISM #formal_name Glycine max #common_name soybean
 DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 ACCESSIONS S33520
 REFERENCE S33520
 #authors Chow, T.; Hsing, Y.C.; Chen, Z.
 #submission submitted to the EMBL Data Library, June 1993
 #description cDNA sequences for a soybean seed maturation polypeptide gene family.
 #accession S33520
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-458 ##label CHO
 ##cross-references EMBL:Z22872
 SUMMARY #length 458 #molecular-weight 49399 #checksum 5605

Query Match 26.6%; Score 77; DB 9; Length 458;
 Best Local Similarity 22.2%; Pred. No. 8.66e-01;
 Matches 8; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Db 181 dyatqktkdyasdatdaakktkdyaqktkdyasda 216
 :| : |:|:|: : :| : | |:|:|:
 Qy 193 QYDNESKKNYGSQPPSSSTSLAQYDSNSKKIYGSQPN 228

Search completed: Mon Feb 3 17:00:21 1997
Job time : 10 secs.

MASPAR (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:59:28 1997; MasPar time 4.51 Seconds
456.034 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4
Description: (296-375) from US08426509.pep (2 of 5)
Perfect Score: 579
Sequence: 1 WFAGNISRSQSEQLLRQKGK.....ENKLYLAENYCFDSIPKLIH 80

Scoring table: PAM 150
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 37.725; Variance 82.158; scale 0.459

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB ID	Description	Pred. No.
1	325	56.1	659	11	I37212	Bruton agammaglobuli	8.36e-39
2	325	56.1	659	11	S28912	protein-tyrosine kin	8.36e-39
3	324	56.0	659	12	B45184	B cell progenitor ki	1.26e-38
4	324	56.0	660	12	JN0471	protein-tyrosine kin	1.26e-38
5	319	55.1	442	11	A45184	B cell progenitor ki	9.71e-38
6	311	53.7	620	4	S33253	protein-tyrosine kin	2.54e-36
7	307	53.0	619	4	JN0472	protein-tyrosine kin	1.29e-35
8	307	53.0	619	4	A47333	T-cell-specific tyro	1.29e-35
9	307	53.0	625	4	A43030	protein-tyrosine kin	1.29e-35
10	300	51.8	527	12	A55631	protein-tyrosine kin	2.21e-34

11	291	50.3	527	4	S13763	protein-tyrosine kin	8.42e-33
12	291	50.3	602	4	JU0215	tyrosine kinase, tec	8.42e-33
13	291	50.3	608	4	JU0227	protein-tyrosine kin	8.42e-33
14	291	50.3	630	4	JU0228	protein tyrosine kin	8.42e-33
15	254	43.9	590	1	TVFFDS	protein-tyrosine kin	2.23e-26
16	166	28.7	499	4	A40092	protein-tyrosine kin	8.32e-12
17	166	28.7	505	1	TVHUHC	protein-tyrosine kin	8.32e-12
18	162	28.0	517	4	A43807	protein-tyrosine kin	3.53e-11
19	161	27.8	537	4	A45501	protein-tyrosine kin	5.05e-11
20	160	27.6	517	12	S24547	protein-tyrosine kin	7.24e-11
21	159	27.5	503	4	J01321	protein-tyrosine kin	1.04e-10
22	159	27.5	503	1	TVMSHC	protein-tyrosine kin	1.04e-10
23	158	27.3	528	1	TVFVG9	protein-tyrosine kin	1.48e-10
24	158	27.3	541	1	TVCHYS	protein-tyrosine kin	1.48e-10
25	158	27.3	543	1	TVHUYS	protein-tyrosine kin	1.48e-10
26	158	27.3	557	10	A00629	protein-tyrosine kin	1.48e-10
27	157	27.1	541	4	A43610	protein-tyrosine kin	2.12e-10
28	157	27.1	541	12	S31645	protein-tyrosine kin	2.12e-10
29	157	27.1	542	1	TVHUSC	protein-tyrosine kin	2.12e-10
30	156	26.9	529	1	TVHUFR	protein-tyrosine kin	3.03e-10
31	155	26.8	526	1	TVFV60	protein-tyrosine kin	4.32e-10
32	155	26.8	533	1	TVCHS	protein-tyrosine kin	4.32e-10
33	155	26.8	539	11	B49114	protein-tyrosine kin	4.32e-10
34	155	26.8	557	1	TVFVS2	protein-tyrosine kin	4.32e-10
35	155	26.8	587	1	TVFVPR	protein-tyrosine kin	4.32e-10
36	154	26.6	663	1	TVNVRR	protein-tyrosine kin	6.16e-10
37	154	26.6	1290	11	A36466	1-phosphatidylinosit	6.16e-10
38	154	26.6	1290	12	A31317	1-phosphatidylinosit	6.16e-10
39	154	26.6	1291	12	S00666	1-phosphatidylinosit	6.16e-10
40	153	26.4	536	4	S33569	protein-tyrosine kin	8.79e-10
41	153	26.4	981	1	FOHVGM	gag-abl polyprotein	8.79e-10
42	153	26.4	1123	4	A39962	kinase-related trans	8.79e-10
43	153	26.4	1130	1	TVHUA	protein-tyrosine kin	8.79e-10
44	152	26.3	526	1	TVFVR	protein-tyrosine kin	1.25e-09
45	152	26.3	568	1	TVFVS1	protein-tyrosine kin	1.25e-09

ALIGNMENTS

```

RESULT      1
ENTRY       I37212      #type complete
TITLE       Bruton agammaglobulinemia tyrosine kinase - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change
              09-Mar-1996
ACCESSIONS  I37212
REFERENCE   I37212
#authors    Dhta, Y.; Haire, R.N.; Litman, R.T.; Fu, S.M.; Nelson, R.P.;
              Kratz, J.; Kornfeld, S.J.; de la Morena, M.; Good, R.A.;
              Litman, G.W.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9062-9066
#title       Genomic organization and structure of Bruton
              agammaglobulinemia tyrosine kinase: localization of
              mutations associated with varied clinical presentations and
              course in X chromosome-linked agammaglobulinemia.
#cross-references NUID:94377492
#accession   I37212
##status     preliminary
##molecule_type DNA
##residues    1-659 ##label RES
##cross-references EMBL:U10087; NID:g517436; CDS_PID:g517438
##note        only intron-exon junctions are shown

GENETICS
#gene        GDB:BTk; AGMX1; IND1
##cross-references GDB:G00-120-542
#map position Xp21.33-n22

```

#introns 47/3; 80/3; 103/3; 131/1; 174/1; 196/3; 259/2; 280/2; 298/3;

325/2; 368/1; 393/1; 450/2; 522/3; 544/2; 584/1; 636/3

SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 56.1%; Score 325; DB 11; Length 659;
Best Local Similarity 48.8%; Pred. No. 8.36e-39;
Matches 39; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhntrsqaeklkkqegkeggfivrdsskagkytvsvfakstgdpqgvirhyvvcstp 340
|:: ::|||:||||:| ||||:|:|:| | :||||:|:|: | | :|| | : :

Qy 296 WFAGNISRSQSEQLLRQKGEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsqqylaekhlfstipelin 360
:: ||||: | :|| ||:

Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 2

ENTRY S28912 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112) atk - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change
01-Dec-1995
ACCESSIONS S28912
REFERENCE S28912
#authors Vetrie, D.; Vorechovsky, I.; Sideras, P.; Holland, J.;
Davies, A.; Flinter, F.; Hammarstroem, L.; Kinnon, C.;
Levinsky, R.; Bobrow, M.; Smith, C.I.E.; Bentley, D.R.
#journal Nature (1993) 361:226-233
#title The gene involved in X-linked agammaglobulinaemia is a member
of the src family of protein-tyrosine kinases.
#accession S28912
##status preliminary
##molecule_type mRNA
##residues 1-659 ##label VET
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
homology
KEYWORDS phosphotransferase
FEATURE
221-269 #domain SH3 homology #label SH3\
281-377 #domain SH2 homology #label SH2\
400-658 #domain protein kinase homology #label KIN
SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 56.1%; Score 325; DB 11; Length 659;
Best Local Similarity 48.8%; Pred. No. 8.36e-39;
Matches 39; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhntrsqaeklkkqegkeggfivrdsskagkytvsvfakstgdpqgvirhyvvcstp 340
|:: ::|||:||||:| ||||:|:|:| | :||||:|:|: | | :|| | : :

Qy 296 WFAGNISRSQSEQLLRQKGEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsqqylaekhlfstipelin 360
:: ||||: | :|| ||:

Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 3

ENTRY B45184 #type complete
TITLE B cell progenitor kinase, BPK=cytoplasmic tyrosine kinase -
mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
12-May-1995
ACCESSIONS B45184
REFERENCE A45184

#authors Tsukada, S.; Saffran, D.C.; Rawlings, D.J.; Parolini, O.;
 Allen, R.C.; Klisak, I.; Sparkes, R.S.; Kubagawa, H.;
 Mohandas, T.; Quan, S.; Belmont, J.W.; Cooper, M.D.;
 Conley, M.E.; Witte, O.N.

#journal Cell (1993) 72:279-290

#title Deficient expression of a B cell cytoplasmic tyrosine kinase
 in human X-linked agammaglobulinemia.

#cross-references MUID:93145329

#accession B45184

##status preliminary; not compared with conceptual translation

##molecule_type nucleic acid

##residues 1-659 ##label TSU

##cross-references NCBIP:123834

##experimental_source 70z/3 pre-B cell line1

##note sequence extracted from NCBI backbone

CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
 homology

FEATURE

221-269 #domain SH3 homology #label SH3\
 281-377 #domain SH2 homology #label SH2\
 400-658 #domain protein kinase homology #label KIN

SUMMARY #length 659 #molecular-weight 76326 #checksum 9917

Query Match 56.0%; Score 324; DB 12; Length 659;
 Best Local Similarity 47.5%; Pred. No. 1.26e-38;
 Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhntsrqaeqlkqegkeggfivrdsskagkytvsvfakstgepggvirhyvvcstp 340
 |:: ::|||:||||:| |||:|:|:| |::|||:|:|: : |::|| |::|
 Qy 296 WFAGNISRSQSEQLLRQKGEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsyyylaekhlfstipelin 360
 :: |||: |::| ||:
 Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 4

ENTRY JN0471 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) emb - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
 12-May-1995

ACCESSIONS JN0471

REFERENCE JN0471

#authors Yanada, N.; Kawakami, Y.; Kimura, H.; Fukamachi, H.; Baier,
 G.; Altman, A.; Kato, T.; Inagaki, Y.; Kawakami, T.

#journal Biochem. Biophys. Res. Commun. (1993) 192:231-240

#title Structure and expression of novel protein-tyrosine kinases,
 Emb and Ent, in the hematopoietic cells.

#accession JN0471

##molecule_type mRNA

##residues 1-660 ##label YAM

##note the nucleotide sequence is not given

GENETICS

#gene emb

CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
 homology

KEYWORDS phosphotransferase

FEATURE

223-271 #domain SH3 homology #label SH3\
 283-379 #domain SH2 homology #label SH2\
 402-659 #domain protein kinase homology #label KIN\
 552 #binding_site phosphate (Tyr) (covalent) #status
 predicted

SUMMARY #length 660 #molecular-weight 76577 #checksum 1680

Query Match 56.0%; Score 324; DB 12; Length 660;
Best Local Similarity 47.5%; Pred. No. 1.26e-38;
Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Db 283 wyskhntsrqaeqlkqegkeggfivrdsskagkytvsvfakstgepqgvirhyvvcstp 342
|:: ::|||:||||:| |||:|:|:| |::|:|:|:| : |::| | : :
Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355

Db 343 qsqqylaekhlfstipelin 362
:: |||: | :| | |:
Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 5

ENTRY A45184 #type fragment
TITLE B cell progenitor kinase - human (fragment)
CONTAINS tyrosine kinase
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
19-Oct-1995
ACCESSIONS A45184
REFERENCE A45184
#authors Tsukada, S.; Saffran, D.C.; Rawlings, D.J.; Parolini, O.;
Allen, R.C.; Klisak, I.; Sparkes, R.S.; Kubagawa, H.;
Mohandas, T.; Guan, S.; Belmont, J.W.; Cooper, M.D.;
Conley, M.E.; Witte, D.N.
#journal Cell (1993) 72:279-290
#title Deficient expression of a B cell cytoplasmic tyrosine kinase
in human X-linked agammaglobulinemia.
#cross-references MUID:93145329
#accession A45184
##status preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-442 ##label TSU
##cross-references NCBIP:123835
##experimental_source erythroleukemia cell line K562
##note sequence extracted from NCBI backbone
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
homology
FEATURE
221-269 #domain SH3 homology #label SH3\
281-377 #domain SH2 homology #label SH2\
400-442 #domain protein kinase homology (fragment) #label KIN
SUMMARY #length 442 #checksum 2964

Query Match 55.1%; Score 319; DB 11; Length 442;
Best Local Similarity 47.5%; Pred. No. 9.71e-38;
Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhntsrqaeqlkqegkeggfivrdsskaakytvsvfakstgdpqgvirhyvvcstp 340
|:: ::|||:||||:| |||:|:|:| |::|:|:|:| : | |::| | : :
Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsqqylaekhlfstipelin 360
:: |||: | :| | |:
Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 6

ENTRY S33253 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change
19-Oct-1995
ACCESSIONS S33253
REFERENCE S33253

CC transformation. Such compounds have value in the treatment of
CC chronic, acute myelogenous or acute lymphocytic leukaemia.
SQ Sequence 1336 AA;

Query Match 7.7%; Score 85; DB 15; Length 1336;
Best Local Similarity 27.3%; Pred. No. 9.62e+00;
Matches 12; Conservative 15; Mismatches 15; Indels 2; Gaps 2;

Db 515 kvqindkddtseykhafeiilkdgnsvifsaksaeeknnuuaal 558
|| :: : | :|:| ||| :::: | :: | ||
Qy 65 KVNLEE-QTPVERQYPFQIVYKDGLLYVYASN-EESRSQWLKAL 106

Search completed: Mon Feb 3 16:54:34 1997
Job time : 30 secs.

MPsrch_pp (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:52:39 1997; MasPar time 6.14 Seconds
607.923 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4
Description: (25-169) from US08426509.pep (1 of 5)
Perfect Score: 1102
Sequence: 1 NYKERLFVLTKTNLSYYEYD.....ANLHTAVNEEKHRVPTFPDR 145

Scoring table: PAM 150
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 41.009; Variance 85.671; scale 0.479

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
--------	-----	-------	-------	--------	----	----	-------------	-----------

1	447	40.6	602	4	JU0215	tyrosine kinase, tec	6.81e-62
2	447	40.6	608	4	JU0227	protein-tyrosine kin	6.81e-62
3	447	40.6	630	4	JU0228	protein tyrosine kin	6.81e-62
4	423	38.4	620	4	S33253	protein-tyrosine kin	2.39e-57
5	413	37.5	619	4	JN0472	protein-tyrosine kin	1.84e-55
6	413	37.5	619	4	A47333	T-cell-specific tyro	1.84e-55
7	368	33.4	625	4	A43030	protein-tyrosine kin	4.92e-47
8	314	28.5	442	11	A45184	B cell progenitor ki	4.39e-37
9	314	28.5	659	11	S28912	protein-tyrosine kin	4.39e-37
10	314	28.5	659	11	I37212	Bruton agammaglobuli	4.39e-37
11	314	28.5	660	12	JN0471	protein-tyrosine kin	4.39e-37
12	313	28.4	659	12	B45184	B cell progenitor ki	6.68e-37
13	225	20.4	847	12	A56039	GTPase-activating pr	2.97e-21
14	202	18.3	527	4	S13763	protein-tyrosine kin	2.46e-17
15	142	12.9	1165	11	A42142	gap1 protein - fruit	1.14e-07
16	142	12.9	1165	10	S27809	GTPase-activating pr	1.14e-07
17	116	10.5	205	7	JU0223	hypothetical 24K pro	7.29e-04
18	98	8.9	350	11	S00755	pleckstrin - human	1.90e-01
19	97	8.8	1042	4	A33881	Ca2+-transporting AT	2.55e-01
20	97	8.8	1042	1	PWRBMC	Ca2+-transporting AT	2.55e-01
21	92	8.3	218	9	S47016	hypothetical protein	1.08e+00
22	91	8.3	348	4	JN0633	caricain (EC 3.4.22.	1.43e+00
23	91	8.3	454	7	B64107	chromosomal replicat	1.43e+00
24	90	8.2	345	1	PPPA	papain (EC 3.4.22.2)	1.89e+00
25	90	8.2	2223	11	A47447	calcium channel prot	1.89e+00
26	88	8.0	549	9	S46029	hypothetical protein	3.29e+00
27	88	8.0	1928	12	JS0610	beta-galactosidase (3.29e+00
28	87	7.9	328	9	S45998	hypothetical protein	4.33e+00
29	86	7.8	458	10	S57605	hypothetical protein	5.68e+00
30	86	7.8	704	14	S61612	hypothetical protein	5.68e+00
31	86	7.8	775	9	S35543	DNA-directed DNA pol	5.68e+00
32	86	7.8	1549	2	A40691	trichohyalin - sheep	5.68e+00
33	85	7.7	97	7	B37141	parC protein - Esche	7.43e+00
34	85	7.7	104	7	B47062	pyocin positive regu	7.43e+00
35	85	7.7	362	12	A38135	ADP-ribosylarginine	7.43e+00
36	85	7.7	807	11	A34581	oxysterol-binding pr	7.43e+00
37	85	7.7	809	12	A34404	oxysterol-binding pr	7.43e+00
38	85	7.7	1336	12	S25716	SOS-1 protein - mous	7.43e+00
39	85	7.7	1487	4	S15904	alpha-1 proteinase i	7.43e+00
40	84	7.6	329	8	H64143	hypothetical protein	9.71e+00
41	83	7.5	305	8	S47261	cheR protein - Rhodo	1.26e+01
42	83	7.5	2009	10	A31068	SEC7 protein - yeast	1.26e+01
43	82	7.4	813	11	B47485	ABR protein 2 - huma	1.64e+01
44	82	7.4	822	11	A47485	ABR protein 1 - huma	1.64e+01
45	82	7.4	1477	4	A29952	alpha-1-inhibitor II	1.64e+01

ALIGNMENTS

```

RESULT      1
ENTRY       JU0215      #type complete
TITLE       tyrosine kinase, tec type II - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
              01-Dec-1995
ACCESSIONS  JU0215
REFERENCE   JU0215
#authors    Mano, H.; Mano, K.; Copeland, N.; Ihle, J.N.
#submission submitted to JIPID, December 1991
#accession  JU0215
##molecule_type mRNA
##residues   1-602 ##label MAN
##experimental_source liver, strain Balb/c
GENETICS
#gene       ter

```

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
KEYWORDS kinase-related transforming protein
FEATURE
185-223 #domain SH3 homology #status atypical #label SH3\
345-602 #domain protein kinase homology #label KIN\
353-361 #region protein kinase ATP-binding motif\
496 #binding_site phosphate (Tyr) (covalent) (by
autophosphorylation) #status predicted
SUMMARY #length 602 #molecular-weight 70103 #checksum 7992

Query Match 40.6%; Score 447; DB 4; Length 602;
Best Local Similarity 45.8%; Pred. No. 6.81e-62;
Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

Db 25 nykerlcvlpksvlsyye-graekkyrkavidiskikcveivknddgvipcqnfqpfqv 83
||||| || | : ||||| : : ||| | : ||: ||| | : : | : : ||| :
Qy 25 NYKERLFVLTKNLSYYEYDKMKRGRKSIEIKKIRCVEKNLEEQT-PVERQYPFQIV 83

Db 84 hdantlyifapspqsrdruvkkllkeeiknnnninikyhpkfwadgsyqccrqteteklapgc 143
||: ||: : || : || | || : | : : ||| : | || : ||: | ||||
Qy 84 YKDGLLYVYASNEESRSQWLKALQKEIRGNPHLLVKYHSGFFVDGKFLCCQSQCAAPGC 143

RESULT 2
ENTRY JU0227 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112) tec III - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
01-Dec-1995
ACCESSIONS JU0227
REFERENCE JU0227
#authors Mano, H.; Sato, K.; Yazaki, Y.; Hirai, H.
#submission submitted to JIPID, March 1993
#description The Tec protein-tyrosine kinase is involved in the IL-3
signaling pathway in a murine myeloid cell line.
#accession JU0227
##molecule_type mRNA
##residues 1-608 ##label MAN
GENETICS
#gene Tec
CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
KEYWORDS kinase-related transforming protein; phosphotransferase
FEATURE
185-223 #domain SH3 homology #status atypical #label SH3\
345-603 #domain protein kinase homology #label KIN\
496 #binding_site phosphate (Tyr) (covalent) #status
predicted
SUMMARY #length 608 #molecular-weight 71162 #checksum 1974

Query Match 40.6%; Score 447; DB 4; Length 608;
Best Local Similarity 45.8%; Pred. No. 6.81e-62;
Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

Db 25 nykerlcvlpksvlsyye-graekkyrkavidiskikcveivknddgvipcqnfqpfqv 83
||||| || | : ||||| : : ||| | : ||: ||| | : : | : : ||| :
Qy 25 NYKERLFVLTKNLSYYEYDKMKRGRKSIEIKKIRCVEKNLEEQT-PVERQYPFQIV 83

Db 84 hdantlyifapspqsrdruvkkllkeeiknnnninikyhpkfwadgsyqccrqteteklapgc 143
||: ||: : || : || | || : | : : ||| : | || : ||: | ||||
Qy 84 YKDGLLYVYASNEESRSQWLKALQKEIRGNPHLLVKYHSGFFVDGKFLCCQSQCAAPGC 143

RESULT 3
ENTRY JU0228 #type complete

TITLE protein tyrosine kinase (EC 2.7.1.-) tec IV - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
 21-Mar-1996
 ACCESSIONS JU0228
 REFERENCE JU0228
 #authors Mano, H.; Sato, K.; Yazaki, Y.; Hirai, H.
 #submission submitted to JIPID, April 1993
 #accession JU0228
 ##molecule_type DNA
 ##residues 1-630 ##label MAN
 ##experimental_source myeloid
 CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase
 homology; SH2 homology; SH3 homology
 KEYWORDS kinase-related transforming protein; phosphotransferase
 FEATURE
 185-233 #domain SH3 homology #label SH3\
 246-344 #domain SH2 homology #label SH2\
 367-625 #domain protein kinase homology #label KIN\
 375-383 #region protein kinase ATP-binding motif\
 515 #active_site Asp (aspartylphosphate intermediate)
 #status predicted
 SUMMARY #length 630 #molecular-weight 73651 #checksum 4354

 Query Match 40.6%; Score 447; DB 4; Length 630;
 Best Local Similarity 45.8%; Pred. No. 6.81e-62;
 Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

Db 25 nykerlcvlpksvlsyye-graekkyrkvidiskikcveivknddgvipcqnkfpfqvv 83
 ||||| || | : |||| : : ||| | : ||: || | : : | : : ||: |
 Qy 25 NYKERLFLVLTKNLSYYEYDKMKRGSRKGSIEIKKIRCVEKNLEEQT-PVERQYPFQIV 83

 Db 84 hdantlyifapspqsrdrwvkkllkeeiknnnnimikyhpkwadgsyqccrqlapgc 143
 ||: ||: : || : || | || : ||: ||: | || : ||: | ||||
 Qy 84 YKDGLLYVYASNEESRSQWLKALQKEIRGNPHLLVKYHSGFFVDGKFLCCQSQSCKAAPGC 143

RESULT 4
 ENTRY S33253 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change
 19-Oct-1995
 ACCESSIONS S33253
 REFERENCE S33253
 #authors Tanaka, N.; Asao, H.; Ohtani, K.; Nakanura, M.; Sugamura, K.
 #journal FEBS Lett. (1993) 324:1-5
 #title A novel human tyrosine kinase gene inducible in T cells by
 interleukin 2.
 #accession S33253
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-620 ##label TAN
 ##cross-references EMBL:D13720
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology
 KEYWORDS phosphotransferase
 FEATURE
 178-226 #domain SH3 homology #label SH3\
 361-619 #domain protein kinase homology #label KIN
 SUMMARY #length 620 #molecular-weight 71830 #checksum 8123

 Query Match 38.4%; Score 423; DB 4; Length 620;
 Best Local Similarity 46.0%; Pred. No. 2.39e-57;
 Matches 57; Conservative 26; Mismatches 41; Indels 0; Gaps 0;

Db 25 nfkvrffvltkaslaufedrghqkrtlkgsielsrikcveivksdisipchukupfqvvh 84

Job time : 9 secs.

MASSIVE (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:02:47 1997; MasPar time 2.55 Seconds
151.211 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-2
Description: (493-507) from US08426509.pep (4 of 4)
Perfect Score: 92
Sequence: 1 GQDADCGSTSPRSQEP 15

Scoring table: PAM 150
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 22.865; Variance 34.220; scale 0.668

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	92	100.0	507	4	A55625	protein-tyrosine kin	4.02e-08	
2	75	81.5	465	4	B55625	protein-tyrosine kin	1.99e-04	
3	75	81.5	465	12	I48926	protein-tyrosine kin	1.99e-04	
4	54	58.7	156	3	Q0BEG9	HHRF1 protein - huma	2.65e+00	
5	54	58.7	755	12	S32103	filensin - bovine	2.65e+00	
6	52	56.5	717	6	S31034	retrovirus-related g	6.01e+00	
7	52	56.5	717	6	S31035	retrovirus-related g	6.01e+00	
8	51	55.4	1004	9	JC2221	major surface glycop	8.99e+00	
9	50	54.3	41	11	A47602	complement C3b/C4b r	1.34e+01	
10	50	54.3	195	11	S31861	myristylated alanine	1.34e+01	
11	50	54.3	200	12	S17185	myristoylated alanin	1.34e+01	
12	50	54.3	226	12	A26964	neuronal growth-rela	1.34e+01	
13	50	54.3	227	12	A29800	neuromodulin - mouse	1.34e+01	

14	50	54.3	545	7	F64181	CTP synthetase (pyrG	1.34e+01
15	50	54.3	2039	11	S03843	complement C3b/C4b r	1.34e+01
16	49	53.3	133	5	S24315	motilin precursor -	1.98e+01
17	49	53.3	351	12	A56387	helix-loop-helix tra	1.98e+01
18	49	53.3	436	7	S13583	nosD protein precurs	1.98e+01
19	49	53.3	471	7	S35635	DNA injection protei	1.98e+01
20	49	53.3	590	12	A40437	glutamic acid-rich p	1.98e+01
21	49	53.3	926	12	A54142	nucleoporin NUP107 -	1.98e+01
22	48	52.2	188	10	S44817	F44E2.2 protein - Ca	2.92e+01
23	48	52.2	559	11	B56731	chromatin assembly f	2.92e+01
24	48	52.2	627	10	A44112	spidroin 2, dragline	2.92e+01
25	48	52.2	1101	8	S15271	endoglucanase cenC -	2.92e+01
26	48	52.2	1396	12	A44453	translation initiati	2.92e+01
27	48	52.2	3566	11	A40701	tenascin-X precursor	2.92e+01
28	47	51.1	179	12	JH0499	glutamine/glutamic a	4.28e+01
29	47	51.1	189	14	D49600	genome-linked protei	4.28e+01
30	47	51.1	190	2	RHSHCE	corticoliberin precu	4.28e+01
31	47	51.1	315	6	D48560	immediate-early prot	4.28e+01
32	47	51.1	332	10	S60935	Lpel7 protein - yeas	4.28e+01
33	47	51.1	357	6	S18236	omega secalin precur	4.28e+01
34	47	51.1	357	6	S18235	omega secalin precur	4.28e+01
35	47	51.1	401	14	S58355	CP49 protein - chick	4.28e+01
36	47	51.1	425	5	A26431	nerve growth factor	4.28e+01
37	47	51.1	427	2	GQHUN	nerve growth factor	4.28e+01
38	47	51.1	450	11	S58351	CP49ins protein - ch	4.28e+01
39	47	51.1	479	11	A34924	complement C3b/C4b r	4.28e+01
40	47	51.1	591	11	A45135	profilaggrin - human	4.28e+01
41	47	51.1	664	2	VEHULA	lamin A - human	4.28e+01
42	47	51.1	713	11	S42803	fibroblast growth fa	4.28e+01
43	47	51.1	775	3	EDBE11	immediate-early prot	4.28e+01
44	47	51.1	1772	10	A45532	major merozoite surf	4.28e+01
45	47	51.1	2248	11	A35938	profilaggrin - human	4.28e+01

ALIGNMENTS

```

RESULT      1
ENTRY       A55625      #type complete
TITLE       protein-tyrosine kinase (EC 2.7.1.112),
            megakaryocyte-associated - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
            01-Mar-1996
ACCESSIONS  A55625; S43533
REFERENCE   A55625
#authors    Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
            L.L.; White, R.A.; Avraham, H.
#journal    J. Biol. Chem. (1995) 270:1833-1842
#title      Structural and functional studies of the intracellular
            tyrosine kinase MATK gene and its translated product.
#accession  A55625
##status    preliminary; not compared with conceptual translation
##molecule_type DNA
##residues  1-507 ##label AVR
REFERENCE   S43533
#authors    Sakano, S.; Iwama, A.; Inazawa, J.; Ariyana, T.; Ohno, M.;
            Suda, T.
#journal    Oncogene (1994) 9:1155-1161
#title      Molecular cloning of a novel non-receptor tyrosine kinase,
            HYL (hematopoietic consensus tyrosine-lacking kinase).
#accession  S43533
##status    preliminary
##molecule_type mRNA
##residues  1-507 ##label SAK
##cross-references EMBL:X77278
GENETICS

```

#gene GDB:MATK
 ##cross-references GDB:G00-304-667
 CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3
 homology
 KEYWORDS phosphotransferase
 FEATURE
 55-105 #domain SH3 homology #label SH31\
 122-211 #domain SH2 homology #label SH2\
 233-485 #domain protein kinase homology #label KIN
 SUMMARY #length 507 #molecular-weight 56469 #checksum 6051

 Query Match 100.0%; Score 92; DB 4; Length 507;
 Best Local Similarity 100.0%; Pred. No. 4.02e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 493 gqdadgstsprsqep 507
 |||||
 Qy 493 GQDADGSTSPRSQEP 507

RESULT 2
 ENTRY B55625 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112),
 megakaryocyte-associated - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
 19-Oct-1995
 ACCESSIONS B55625
 REFERENCE A55625
 #authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
 L.L.; White, R.A.; Avraham, H.
 #journal J. Biol. Chem. (1995) 270:1833-1842
 #title Structural and functional studies of the intracellular
 tyrosine kinase MATK gene and its translated product.
 #accession B55625
 ##status preliminary; not compared with conceptual translation
 ##molecule_type mRNA
 ##residues 1-465 ##label AVR
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
 homology
 KEYWORDS phosphotransferase
 FEATURE
 13-63 #domain SH3 homology #label SH31\
 80-169 #domain SH2 homology #label SH2\
 191-443 #domain protein kinase homology #label KIN
 SUMMARY #length 465 #molecular-weight 51585 #checksum 6919

 Query Match 81.5%; Score 75; DB 4; Length 465;
 Best Local Similarity 60.0%; Pred. No. 1.99e-04;
 Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 451 gqeaegsaptrsqp 465
 ||:|:|:|:|
 Qy 493 GQDADGSTSPRSQEP 507

RESULT 3
 ENTRY I48926 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
 ALTERNATE_NAMES csk-type protein-tyrosine kinase
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
 15-Mar-1996
 ACCESSIONS I48926
 REFERENCE A53469
 #authors Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.;

CC to SH2 regions of Src, Abl, Lck and p85-alpha-N (R72088-91,
CC respectively).
SQ Sequence 99 AA;

Query Match 31.7%; Score 187; DB 13; Length 99;
Best Local Similarity 32.9%; Pred. No. 1.98e-09;
Matches 25; Conservative 23; Mismatches 27; Indels 1; Gaps 1;


```

Db      5 wyugdisreevnek1rldtadgtflvrdestknhgdytltlrkggnnklikifhrdgkygf 64
      | : | | : | : | : | | | | : : | | | : | : : : | | | :
Qy     122 WFHGKISGQEA VQQLQPPEDGLFLVRE-SARHPGDYVLCVSFGRDVIHYRVLHRDGH LTI 180

Db      65 sdpltfnsvvelinhy 80
      : : | : : : : : | |
Qy     181 DEAVFFCNLM DMVEHY 196

```

Search completed: Mon Feb 3 17:02:02 1997
Job time : 6 secs.



(TM)

Release 2.1D John F. Collins; Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

```
Run on:      Mon Feb 3 17:01:07 1997; MasPar time 4.29 Seconds
                                         450.074 Million cell updates/sec
Tabular output not generated.
```

```
Title:                >US-08-426-509-2
Description:          (122-196) from US08426509.pep (3 of 4)
Perfect Score:       590
Sequence:            1 WFHGKISGQEA VQQLPPED.....HLTIDEAVFFCNLMQVVEHY 75
```

Scoring table: PAM 150
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database:      pir48
               1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
               8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
               14:unrev
```

Statistics: Mean 38.199; Variance 81.461; scale 0.469

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB	ID	Description	Pred. No.
	No.	Score	Match	Length				
1	590	100.0	507	4	A55625	protein-tyrosine kin	4.42e-89	
2	590	100.0	527	11	A49865	protein-tyrosine kin	4.42e-89	
3	570	96.6	465	4	B55625	protein-tyrosine kin	2.92e-85	
4	570	96.6	465	12	I48926	protein-tyrosine kin	2.92e-85	
5	350	59.3	450	1	JH0559	protein-tyrosine kin	5.07e-44	
6	349	59.2	450	12	I48929	protein-tyrosine kin	7.73e-44	
7	349	59.2	450	1	S15094	protein-tyrosine kin	7.73e-44	
8	344	58.3	450	4	A41973	protein-tyrosine kin	6.33e-43	
9	215	36.4	723	12	B38749	3-phosphatidylinosit	4.48e-20	
10	202	34.2	451	12	S49016	tyrosine kinase - hu	7.01e-18	
11	199	33.7	217	12	A54688	modular adaptor Grb2	2.23e-17	
12	199	33.7	217	11	A43321	growth factor recept	2.23e-17	
13	199	33.7	217	12	S26050	gene ash protein - r	2.23e-17	
14	195	33.1	841	11	A43254	protein-tyrosine-pho	1.04e-16	
15	194	32.9	217	11	JT0664	growth factor recept	1.52e-16	
16	192	32.5	724	11	A38748	3-phosphatidylinosit	3.27e-16	
17	191	32.4	239	12	A46243	epidermal growth fac	4.79e-16	
18	191	32.4	612	11	JC2197	protein-tyrosine kin	4.79e-16	
19	191	32.4	635	11	JC2198	protein-tyrosine kin	4.79e-16	
20	191	32.4	635	11	A53596	protein-tyrosine kin	4.79e-16	
21	187	31.7	628	12	S57436	protein-tyrosine kin	2.19e-15	
22	187	31.7	724	12	A38747	phosphatidylinositol	2.19e-15	
23	187	31.7	724	12	A38749	3-phosphatidylinosit	2.19e-15	
24	185	31.4	204	5	B45022	CRK-I - human	4.68e-15	
25	185	31.4	304	5	A45022	CRK-II - human	4.68e-15	
26	180	30.5	303	5	S41754	CRKL protein - human	3.09e-14	
27	180	30.5	605	12	B56707	protein-tyrosine kin	3.09e-14	
28	180	30.5	628	12	A56707	protein-tyrosine kin	3.09e-14	
29	178	30.2	303	12	S58352	SH2/SH3 adaptor prot	6.56e-14	
30	178	30.2	557	10	A00629	protein-tyrosine kin	6.56e-14	
31	174	29.5	209	11	A48090	alpha 2-chimerin, p4	2.93e-13	
32	173	29.3	870	11	B40121	GTPase-activating pr	4.26e-13	
33	173	29.3	1047	11	A40121	GTPase-activating pr	4.26e-13	
34	172	29.2	1038	12	JT0663	ras GTPase-activatin	6.18e-13	
35	172	29.2	1044	12	S01966	GTPase-activating pr	6.18e-13	
36	171	29.0	535	12	C46243	epidermal growth fac	8.96e-13	
37	169	28.6	505	4	S24550	protein-tyrosine kin	1.88e-12	
38	166	28.1	443	12	B53764	beta2-chimaerin, cer	5.70e-12	
39	166	28.1	466	11	A53764	beta2-chimaerin, cer	5.70e-12	
40	166	28.1	628	12	A40802	protein-tyrosine kin	5.70e-12	
41	164	27.8	1236	10	A53970	1-phosphatidylinosit	1.19e-11	
42	162	27.5	232	2	TVFV10	transforming protein	2.48e-11	
43	162	27.5	305	5	A49011	c-Crk - chicken	2.48e-11	
44	161	27.3	211	10	A46444	SH2-SH3 adaptor prot	3.57e-11	
45	161	27.3	595	4	A55651	protein-tyrosine-pho	3.57e-11	

ALIGNMENTS

RESULT 1
 ENTRY A55625 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112),
 megakaryocyte-associated - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
 01-Mar-1996
 ACCESSIONS A55625; S43533
 REFERENCE A55625
 #authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
 L.L.; White, R.A.; Avraham, H.
 #journal J. Biol. Chem. (1995) 270:18771-1882

#title Structural and functional studies of the intracellular
 tyrosine kinase MATK gene and its translated product.
 #accession A55625
 ##status preliminary; not compared with conceptual translation
 ##molecule_type DNA
 ##residues 1-507 ##label AVR
 REFERENCE S43533
 #authors Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.;
 Suda, T.
 #journal Oncogene (1994) 9:1155-1161
 #title Molecular cloning of a novel non-receptor tyrosine kinase,
 HYL (hematopoietic consensus tyrosine-lacking kinase).
 #accession S43533
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-507 ##label SAK
 ##cross-references EMBL:X77278
 GENETICS
 #gene GDB:MATK
 ##cross-references GDB:G00-304-667
 CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3
 homology
 KEYWORDS phosphotransferase
 FEATURE
 55-105 #domain SH3 homology #label SH31\
 122-211 #domain SH2 homology #label SH2\
 233-485 #domain protein kinase homology #label KIN
 SUMMARY #length 507 #molecular-weight 56469 #checksum 6051

Query Match 100.0X; Score 590; DB 4; Length 507;
 Best Local Similarity 100.0X; Pred. No. 4.42e-89;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 122 wfhgkisgqeavqqlqppedglflvresarhpgdyvlcvsfgrdvihyrvlhrdghltid 181
 |||
 Qy 122 WFHGKISGQEAVQQLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHILTID 181
 Db 182 eavffcnlmdmavehy 196
 |||
 Qy 182 EAVFFCNLMDMVEHY 196

RESULT 2

ENTRY A49865 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) matk - human
 ALTERNATE_NAMES megakaryocyte-associated tyrosine kinase
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change
 19-Oct-1995
 ACCESSIONS A49865
 REFERENCE A49865
 #authors Bennett, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.;
 Grabarek, J.; Groopman, J.E.; Goeddel, D.V.; Avraham, H.
 #journal J. Biol. Chem. (1994) 269:1068-1074
 #title Identification and characterization of a novel tyrosine
 kinase from megakaryocytes.
 #accession A49865
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-527 ##label BEN
 ##cross-references GB:L18974
 CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3
 homology
 KEYWORDS phosphotransferase
 FEATURE
 55-105 #domain SH3 homology #label SH31\

122-211 #domain SH2 homology #label SH2\
233-484 #domain protein kinase homology #label KIN
SUMMARY #length 527 #molecular-weight 58473 #checksum 1630

Query Match 100.0%; Score 590; DB 11; Length 527;
Best Local Similarity 100.0%; Pred. No. 4.42e-89;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 122 wfhgkisgqeavqqlppedglflvresarhpgdyvlcvsfgrdvihyrvlhrdghltid 181
|||||

Qy 122 WFHGKISGQEAVQQLPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHILTID 181

Db 182 eavffcnlmdmvehy 196
|||||

Qy 182 EAVFFCNLMDMVEHY 196

RESULT 3

ENTRY B55625 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112),
megakaryocyte-associated - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
19-Oct-1995
ACCESSIONS B55625
REFERENCE A55625
#authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,
L.L.; White, R.A.; Avraham, H.
#journal J. Biol. Chem. (1995) 270:1833-1842
#title Structural and functional studies of the intracellular
tyrosine kinase MATK gene and its translated product.
#accession B55625
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-465 ##label AVR
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
homology
KEYWORDS phosphotransferase

FEATURE

13-63 #domain SH3 homology #label SH31\
80-169 #domain SH2 homology #label SH2\
191-443 #domain protein kinase homology #label KIN

SUMMARY #length 465 #molecular-weight 51585 #checksum 6919

Query Match 96.6%; Score 570; DB 4; Length 465;
Best Local Similarity 97.3%; Pred. No. 2.92e-85;
Matches 73; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 80 wfhgkisgqeaiqqlppedglflvresarhpgdyvlcvsfgrdvihyrvlhrdghltid 139
|||||

Qy 122 WFHGKISGQEAVQQLPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHILTID 181

Db 140 eavfcfnlmdmvehy 154
|||

Qy 182 EAVFFCNLMDMVEHY 196

RESULT 4

ENTRY 148926 #type complete
TITLE protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse
ALTERNATE_NAMES csk-type protein-tyrosine kinase
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
15-Mar-1996
ACCESSIONS 148926

REFERENCE A53469

#authors Klages, S.; Adam, D.; Class, K.; Fagnoli, J.; Bolen, J.B.;
 Penhallow, R.C.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2597-2601
 #title Ctk: a protein-tyrosine kinase related to Csk that defines an
 enzyme family.
 #cross-references MUID:94195789
 #accession 148926
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-465 ##label RES
 ##cross-references EMBL:U05210; NID:g450232; CDS_PID:g450233
 KEYWORDS phosphotransferase
 SUMMARY #length 465 #molecular-weight 51495 #checksum 6748

Query Match 96.6%; Score 570; DB 12; Length 465;
 Best Local Similarity 97.3%; Pred. No. 2.92e-85;
 Matches 73; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 80 wfhgkisgqaeaiqlppedglflvresarhpgdyvlcvsfgrdvihyrvlhrdghltid 139
 |||||:|||||
 Qy 122 WFHGKISGQAEAVQQLGPPEDGLFLVRESARHPCDYVLCVSFGRDVIHYRVLHRDGHILTID 181
 Db 140 eavcfcnlmdmavehy 154
 |||||
 Qy 182 EAVFFCNLMDMVEHY 196

RESULT 5

ENTRY JH0559 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) CSK - human
 ALTERNATE_NAMES protein-tyrosine kinase cyl; protein-tyrosine kinase T2
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 30-Jun-1992 #sequence_revision 20-Aug-1994 #text_change
 16-Feb-1996
 ACCESSIONS JH0559; S38818; S19024; S19025
 REFERENCE JH0559
 #authors Braeuninger, A.; Holtrich, U.; Strebhardt, K.;
 Ruebsaen-Waigmann, H.
 #journal Gene (1992) 110:205-211
 #title Isolation and characterization of a human gene that encodes a
 new subclass of protein tyrosine kinases.
 #cross-references MUID:92165060
 #accession JH0559
 ##molecule_type mRNA
 ##residues 1-450 ##label BRA
 ##cross-references EMBL:X59932
 ##experimental_source lung
 REFERENCE S38818
 #authors Braeuninger, A.; Karn, T.; Strebhardt, K.;
 Ruebsaen-Waigmann, H.
 #journal Oncogene (1993) 8:1365-1369
 #title Characterization of the human CSK locus.
 #accession S38818
 ##status preliminary
 ##molecule_type DNA
 ##residues 1-450 ##label BR2
 ##cross-references EMBL:X74765
 REFERENCE S19024
 #authors Partanen, J.; Armstrong, E.; Bergman, M.; Maekela, T.P.;
 Hirvonen, H.; Huebner, K.; Alitalo, K.
 #journal Oncogene (1991) 6:2013-2018
 #title cyl encodes a putative cytoplasmic tyrosine kinase lacking
 the conserved tyrosine autophosphorylation site (Y416
 (src)).
 #cross-references MUID:92050797
 #accession S19024

Run on: Mon Feb 3 17:11:18 1997; MasPar time 9.20 Seconds
671.122 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-6
Description: (247-486) from US08426509.pep (3 of 3)
Perfect Score: 1791
Sequence: 1 GSGQFGEVWGLWNNTTPVA.....QFYINIMLECWNAEPKERPTF 240

Scoring table: PAM 150
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev

Statistics: Mean 45.069; Variance 114.513; scale 0.394

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1775	99.1	505	11	I38396	protein-tyrosine kin	8.20e-266	
2	1272	71.0	505	4	S24550	protein-tyrosine kin	2.96e-182	
3	1268	70.8	506	4	S24553	protein-tyrosine kin	1.35e-181	
4	1203	67.2	362	4	S24551	protein-tyrosine kin	7.25e-171	
5	1189	66.4	334	4	S24552	protein-tyrosine kin	1.47e-168	
6	1114	62.2	509	1	TVHAST	protein-tyrosine kin	3.27e-156	
7	1089	60.8	507	4	A39939	protein-tyrosine kin	4.20e-152	
8	1074	60.0	536	4	S33569	protein-tyrosine kin	1.22e-149	
9	1070	59.7	512	4	A39719	protein-tyrosine kin	5.54e-149	
10	1070	59.7	512	1	TVHULY	protein-tyrosine kin	5.54e-149	
11	1063	59.4	539	11	B49114	protein-tyrosine kin	7.81e-148	
12	1060	59.2	542	11	A49114	protein-tyrosine kin	2.43e-147	
13	1056	59.0	532	4	A34104	protein-tyrosine kin	1.10e-146	
14	1056	59.0	532	4	B34104	protein-tyrosine kin	1.10e-146	
15	1051	58.7	505	1	TVHUNC	protein-tyrosine kin	7.27e-146	
16	1051	58.7	542	1	TVHUSC	protein-tyrosine kin	7.27e-146	
17	1049	58.6	541	4	A43610	protein-tyrosine kin	1.55e-145	
18	1045	58.3	526	4	S15582	protein-tyrosine kin	7.00e-145	
19	1044	58.3	557	1	TVFVS2	protein-tyrosine kin	1.02e-144	
20	1044	58.3	587	1	TVFVPR	protein-tyrosine kin	1.02e-144	
21	1043	58.2	526	1	TVFV60	protein-tyrosine kin	1.49e-144	
22	1042	58.2	526	1	TVFVR	protein-tyrosine kin	2.17e-144	
23	1043	58.2	533	1	TVCHS	protein-tyrosine kin	1.49e-144	
24	1040	58.1	503	1	TVMSHC	protein-tyrosine kin	4.63e-144	
25	1040	58.1	537	4	A43806	protein-tyrosine kin	4.63e-144	
26	1039	58.0	526	4	S20808	protein-tyrosine kin	6.75e-144	
27	1039	58.0	526	1	OKFVYR	protein-tyrosine kin	6.75e-144	
28	1038	58.0	568	1	TVFVS1	protein-tyrosine kin	9.84e-144	
29	1037	57.9	509	4	A23639	protein-tyrosine kin	1.44e-143	
30	1035	57.8	503	4	J01321	protein-tyrosine kin	3.05e-143	
31	1036	57.8	537	1	TVHUSY	protein-tyrosine kin	2.09e-143	
32	1034	57.7	392	4	S04205	protein-tyrosine kin	4.45e-143	

33	1034	57.7	523	1	TVFVMT	protein-tyrosine kin	4.45e-143
34	1032	57.6	526	7	S20676	protein-tyrosine kin	9.47e-143
35	1032	57.6	526	7	S26420	src protein - Rous s	9.47e-143
36	1030	57.5	509	1	OKHULK	protein-tyrosine kin	2.02e-142
37	1029	57.5	537	1	TVHUSR	protein-tyrosine kin	2.94e-142
38	1026	57.3	663	1	TVMVRR	protein-tyrosine kin	9.12e-142
39	1024	57.2	529	1	TVHUFR	protein-tyrosine kin	1.94e-141
40	1022	57.1	517	12	S24547	protein-tyrosine kin	4.12e-141
41	1022	57.1	541	1	TVCHYS	protein-tyrosine kin	4.12e-141
42	1023	57.1	545	7	S52313	pp62v protein - Rous	2.83e-141
43	1022	57.1	546	7	S52314	pp62v protein - Rous	4.12e-141
44	1016	56.7	537	4	A45501	protein-tyrosine kin	3.96e-140
45	1016	56.7	541	12	S31645	protein-tyrosine kin	3.96e-140

ALIGNMENTS

RESULT 1

ENTRY I38396 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human
 ALTERNATE_NAMES FYN-related kinase (FRK)
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 15-Mar-1996
 ACCESSIONS I38396
 REFERENCE I38396
 #authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.
 #journal Gene (1994) 138:247-251
 #title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.
 #cross-references MUID:94171047
 #accession I38396
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-505 ##label RES
 ##cross-references EMBL:U00803; NID:g392887; CDS_PID:g392888
 GENETICS
 #gene GDB:FRK
 ##cross-references GDB:G00-355-675
 KEYWORDS phosphotransferase
 SUMMARY #length 505 #molecular-weight 58254 #checksum 9379

Query Match 99.1%; Score 1775; DB 11; Length 505;
 Best Local Similarity 99.6%; Pred. No. 8.20e-266;
 Matches 239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db	241	gsgqfgevewglwnnttpvavktlkpgsmdpndflreaqimknlrhpkliqlyavctled	300
Qy	247	GSGQFGEVWEGLWNNTPVAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAVCTLED	306
Db	301	piyiitelmrhgslqeylqndtgskihltqqvdnaaqvasgnaylesrnyihrdlaarnv	360
Qy	307	PIYIITELMRHGSLQEYLQNDTGSKIHLTQQYDMAAQVASGNAYLESRNYIHRDLAARNV	366
Db	361	lvgehniykvadfglarvfkvdnediyesrheiklpvkwtapeairsnkfsiksdvwsfg	420
Qy	367	LVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSDVWSFG	426
Db	421	illyeiitygkmpysgmtgaqviqlaagnyrlpqpsncpqfynimlecwnaepkerptf	480
Qy	427	ILLYEIITYGKMPYSGMTGAQVIQLAAGNYRLPQPSNCPQGFYNIMLECWNAEPKERPTF	486

RESULT 2

ENTRY S24550 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) 1 - freshwater sponge

(Spongilla lacustris)

ALTERNATE_NAMES src-type tyrosine kinase 1
 ORGANISM #formal_name Spongilla lacustris
 DATE 07-May-1993 #sequence_revision 07-May-1993 #text_change
 03-Nov-1995

ACCESSIONS S24550
 REFERENCE S24550
 #authors Raulf, F.
 #submission submitted to the EMBL Data Library, September 1991
 #accession S24550
 ##molecule_type mRNA
 ##residues 1-505 ##label RAU
 ##cross-references EMBL:X61601

GENETICS
 #gene srk1

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase
 homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE
 61-111 #domain SH3 homology #label SH3\
 122-214 #domain SH2 homology #label SH2\
 238-496 #domain protein kinase homology #label KIN\
 246-254 #region protein kinase ATP-binding motif\
 268 #active_site Lys #status predicted

SUMMARY #length 505 #molecular-weight 57693 #checksum 3389

Query Match 71.0%; Score 1272; DB 4; Length 505;
 Best Local Similarity 67.5%; Pred. No. 2.96e-182;
 Matches 162; Conservative 40; Mismatches 34; Indels 4; Gaps 3;

Db 247 gagqfgevweglungttsvavktlkpgtmsveeflqeasimkrlrhpqliqlyavctkee 306
 |:||||||| |:|||||||:| :||:| ||| ||||||||| |:|
 Qy 247 GSGQFGEVWEGLNNTTPVAVKTLKPGSMDPNDFLEAQMKNLRHPKLIQLYAVCTLED 306

Db 307 piyivtelmkyslleylrgedgv-lkieqlvdvaaqvasgmsyleqqnyihrdlaarni 365
 ||||:||||: ||| |||:| :| :| |:|||||||:||| :|||||||:
 Qy 307 PIYIITELMRHGSLEQYLQNDTGSKIHLTQYDMAAQVASGMAYLESRYIHRDLAARNV 366

Db 366 lvgehgickvadfglarv--id-eeiyeahtgakfpikwtapeaanyrftiksdvwsfg 422
 ||||| | ||||||||| :| |:|||:| |:|:||||||| |:|:|||||||
 Qy 367 LVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSDVWSFG 426

Db 423 vlyeiitygrfpypgmtnpvlekiqqnyrmpcpncpkqfhdmldcwredpasrptf 482
 ::||||||| |:||| :|:|:| ||||:| |:||| ||| :||:| | :| ||||
 Qy 427 ILLYEIITYGKMPYSGNTGAQVIQMLAQNYRLPQPSNCPQQFYNIIMLECWNAEPKERPTF 486

RESULT 3

ENTRY S24553 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) 4 - freshwater sponge
 (Spongilla lacustris)

ALTERNATE_NAMES src-type tyrosine kinase 4
 ORGANISM #formal_name Spongilla lacustris
 DATE 07-May-1993 #sequence_revision 07-May-1993 #text_change
 03-Nov-1995

ACCESSIONS S24553
 REFERENCE S24550
 #authors Raulf, F.
 #submission submitted to the EMBL Data Library, September 1991
 #accession S24553
 ##molecule_type mRNA
 ##residues 1-506 ##label RAU
 ##cross-references EMBL:X61604

GENETICS
 #gene srk4

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase

homology; SH2 homology; SH3 homology
 KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase
 FEATURE
 61-111 #domain SH3 homology #label SH3\
 122-214 #domain SH2 homology #label SH2\
 238-496 #domain protein kinase homology #label KIN\
 246-254 #region protein kinase ATP-binding motif\
 268 #active_site Lys #status predicted
 SUMMARY #length 506 #molecular-weight 57561 #checksum 9002

Query Match 70.8%; Score 1268; DB 4; Length 506;
 Best Local Similarity 66.7%; Pred. No. 1.35e-181;
 Matches 160; Conservative 40; Mismatches 36; Indels 4; Gaps 3;

Db 247 gagqfgevweglungttsvavktlkpgtmsieefleeasimkqlrhpqliqlyavctkee 306
 |:||||| |:|||||:| :|| ||| ||||| |:|
 Qy 247 GSGQFGEVWEGLNNTTPVAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAVCTLED 306

Db 307 piyivtelmkhgsllleylrgd-grsklpdlvdacsqvasgmsyleqqnyihrdlaarni 365
 ||||:||||:|||| |:| | : | : || :||||:| | :|||||:|
 Qy 307 PIYIITELMRHGSLEQYLQNDTGSKIHLTQQYDMAAQVASGMAYLESRNYIHRDLAARNV 366

Db 366 lvgehkickvadfglarv--id-eeiyeaklgakfpikutapeaanysrftiksdvwsfg 422
 ||||:| ||||| |:| |:|:| |:|:| |:|:| |:|:|
 Qy 367 LVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSDVWSFG 426

Db 423 ivlyevitygrfpypgmtnaqvleqiqqsyrrprmgcpeklgammaadwredpasrptf 482
 |:|:|:| |:|:| |:|:| : |:|:| |:|:| |:|:| |:|:| |:|
 Qy 427 ILLYEIITYGKMPYSGMTGAQVIQMLAQNYRLPQPSNCPQGFYNIMLECWNAEPKERPTF 486

RESULT 4
 ENTRY S24551 #type fragment
 TITLE protein-tyrosine kinase (EC 2.7.1.112) 2 - freshwater sponge
 (Spongilla lacustris) (fragment)
 ALTERNATE_NAMES src-type tyrosine kinase 2
 ORGANISM #formal_name Spongilla lacustris
 DATE 07-May-1993 #sequence_revision 07-May-1993 #text_change
 03-Nov-1995
 ACCESSIONS S24551
 REFERENCE S24550
 #authors Raulf, F.
 #submission submitted to the EMBL Data Library, September 1991
 #accession S24551
 ##molecule_type mRNA
 ##residues 1-362 ##label RAU
 ##cross-references EMBL:X61602

GENETICS
 #gene srk2
 CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase
 homology; SH2 homology; SH3 homology
 KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase
 FEATURE
 1-70 #domain SH2 homology (fragment) #label SH2\
 93-351 #domain protein kinase homology #label KIN\
 101-109 #region protein kinase ATP-binding motif\
 123 #active_site Lys #status predicted
 SUMMARY #length 362 #checksum 2776

Query Match 67.2%; Score 1203; DB 4; Length 362;
 Best Local Similarity 64.6%; Pred. No. 7.25e-171;
 Matches 155; Conservative 44; Mismatches 37; Indels 4; Gaps 4;

Db 102 gagqfgevvyqglunnstpvavktlkagtnqpaaflaeqimkklrhpqliqlyavctqge 161
 |:||||| |:|||||:| |:| ||| ||||| |:|
 Qy 247 GSGQFGEVWEGLNNTTPVAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAVCTLED 306

3	170	38.6	532	4	B34104	protein-tyrosine kin	1.33e-12
4	167	38.0	542	11	A49114	protein-tyrosine kin	3.92e-12
5	166	37.7	534	4	A44991	protein-tyrosine kin	5.62e-12
6	166	37.7	534	4	S33568	protein-tyrosine kin	5.62e-12
7	166	37.7	537	1	TVHUSY	protein-tyrosine kin	5.62e-12
8	166	37.7	537	1	TVHUSR	protein-tyrosine kin	5.62e-12
9	166	37.7	537	4	A45501	protein-tyrosine kin	5.62e-12
10	165	37.5	532	4	A34104	protein-tyrosine kin	8.04e-12
11	165	37.5	537	4	A43806	protein-tyrosine kin	8.04e-12
12	165	37.5	543	1	TVHUYS	protein-tyrosine kin	8.04e-12
13	162	36.8	541	12	S31645	protein-tyrosine kin	2.36e-11
14	161	36.6	517	12	S24547	protein-tyrosine kin	3.37e-11
15	160	36.4	528	1	TVFVG9	protein-tyrosine kin	4.81e-11
16	160	36.4	529	1	TVHUFR	protein-tyrosine kin	4.81e-11
17	160	36.4	541	1	TVCHYS	protein-tyrosine kin	4.81e-11
18	158	35.9	533	1	TVCHS	protein-tyrosine kin	9.79e-11
19	158	35.9	539	11	B49114	protein-tyrosine kin	9.79e-11
20	158	35.9	557	1	TVFVS2	protein-tyrosine kin	9.79e-11
21	158	35.9	568	1	TVFVS1	protein-tyrosine kin	9.79e-11
22	158	35.9	587	1	TVFVPR	protein-tyrosine kin	9.79e-11
23	157	35.7	451	12	S49016	tyrosine kinase - hu	1.40e-10
24	156	35.5	536	4	S33569	protein-tyrosine kin	1.99e-10
25	153	34.8	505	4	S24550	protein-tyrosine kin	5.73e-10
26	153	34.8	506	4	S24553	protein-tyrosine kin	5.73e-10
27	153	34.8	517	4	A43807	protein-tyrosine kin	5.73e-10
28	152	34.5	512	4	A39719	protein-tyrosine kin	8.14e-10
29	151	34.3	526	4	S20808	protein-tyrosine kin	1.16e-09
30	151	34.3	526	4	S15582	protein-tyrosine kin	1.16e-09
31	151	34.3	526	1	TVFVR	protein-tyrosine kin	1.16e-09
32	151	34.3	526	1	DKFVYR	protein-tyrosine kin	1.16e-09
33	147	33.4	505	1	TVHUHC	protein-tyrosine kin	4.68e-09
34	146	33.2	526	1	TVFV60	protein-tyrosine kin	6.62e-09
35	145	33.0	907	9	A57087	cell division contro	9.37e-09
36	144	32.7	503	1	TVMSHC	protein-tyrosine kin	1.32e-08
37	144	32.7	512	1	TVHULY	protein-tyrosine kin	1.32e-08
38	143	32.5	526	7	S20676	protein-tyrosine kin	1.87e-08
39	143	32.5	526	7	S26420	src protein - Rous s	1.87e-08
40	142	32.3	503	4	J01321	protein-tyrosine kin	2.64e-08
41	140	31.8	545	7	S52313	pp62v protein - Rous	5.25e-08
42	140	31.8	546	7	S52314	pp62v protein - Rous	5.25e-08
43	131	29.8	303	5	S41754	CRKL protein - human	1.12e-06
44	130	29.5	259	5	A44988	transforming protein	1.56e-06
45	130	29.5	305	5	A49011	c-Crk - chicken	1.56e-06

ALIGNMENTS

RESULT 1

ENTRY I38396 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human

ALTERNATE_NAMES FYN-related kinase (FRK)

ORGANISM #formal_name Homo sapiens #common_name man

DATE 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 15-Mar-1996

ACCESSIONS I38396

REFERENCE I38396

#authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.

#journal Gene (1994) 138:247-251

#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.

#cross-references MUID:94171047

#accession I38396

##status preliminary

##molecule_type mRNA

##residues 1-505 ##label RES

##cross-references EMBL:U00803; NID:a392887; CDS PID:a392888

ACCESSIONS B34104
 REFERENCE A34104
 #authors Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.
 #journal J. Biol. Chem. (1989) 264:10649-10653
 #title The two *Xenopus laevis* SRC genes are co-expressed and each produces functional pp(60src).
 #cross-references MUID:89278134
 #accession B34104
 ##status preliminary; not compared with conceptual translation
 ##molecule_type mRNA
 ##residues 1-532 ##label STE
 CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase
 FEATURE
 87-136 #domain SH3 homology #label SH3\
 147-244 #domain SH2 homology #label SH2\
 264-522 #domain protein kinase homology #label KIN\
 272-280 #region protein kinase ATP-binding motif
 SUMMARY #length 532 #molecular-weight 59736 #checksum 7595

Query Match 38.6%; Score 170; DB 4; Length 532;
 Best Local Similarity 50.0%; Pred. No. 1.33e-12;
 Matches 19; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

Db 87 alydyesrtetdlsfrkger-lqivnnategdwuarsl 123
 ||:|:|:| | | | | | : | : | : | | : | | |
 Qy 54 ALFDYQARTAEDLSFRAGDKKLQVLDLHEGWWFARHL 91

RESULT 4
 ENTRY A49114 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) fyn - Pacific electric ray
 ORGANISM #formal_name *Torpedo californica* #common_name Pacific electric ray
 DATE 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 19-Jan-1996
 ACCESSIONS A49114
 REFERENCE A49114
 #authors Swope, S.L.; Huganir, R.L.
 #journal J. Biol. Chem. (1993) 268:25152-25161
 #title Molecular cloning of two abundant protein tyrosine kinases in *Torpedo* electric organ that associate with the acetylcholine receptor.
 #accession A49114
 ##status preliminary
 ##molecule_type mRNA
 ##residues 1-542 ##label SWO
 ##cross-references GB:U01349
 CLASSIFICATION #superfamily protein kinase homology; SH3 homology
 KEYWORDS phosphotransferase
 FEATURE
 94-143 #domain SH3 homology #label SH3\
 274-532 #domain protein kinase homology #label KIN
 SUMMARY #length 542 #molecular-weight 61096 #checksum 2657

Query Match 38.0%; Score 167; DB 11; Length 542;
 Best Local Similarity 51.3%; Pred. No. 3.92e-12;
 Matches 20; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

Db 94 alydydartdddlsfhkgek-fqilnntegdwuearsiq 131
 ||:|:|:| | :| | | | | : | : | : | | | | |
 Qy 54 ALFDYQARTAEDLSFRAGDKKLQVLDLHEGWWFARHLE 92

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

```
Run on:      Mon Feb 3 16:55:24 1997; MasPar time 4.55 Seconds
            452.373 Million cell updates/sec
```

```
Title:          >US-08-426-509-6
Description:    (122-201) from US08426509.pep (1 of 3)
Perfect Score: 586
Sequence:      1 WFFGAIGRSDAEKQLLYSEN.....FLTRRRIFSTLNEFVSHYTK 80
```

```
Database:      pir48
               1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
               8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
               14:unrev
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	%		Query		DB		ID	Description	Pred. No.
No.	Score	Match	Length	DB	ID				
1	586	100.0	505	11	I38396		protein-tyrosine kin	4.99e-80	
2	351	59.9	499	4	A40092		protein-tyrosine kin	8.16e-40	
3	347	59.2	509	1	TVHAST		protein-tyrosine kin	3.78e-39	
4	344	58.7	506	4	S24553		protein-tyrosine kin	1.19e-38	
5	334	57.0	505	4	S24550		protein-tyrosine kin	5.45e-37	
6	333	56.8	505	11	S51647		protein-tyrosine kin	7.98e-37	
7	325	55.5	505	1	TVHUHC		protein-tyrosine kin	1.68e-35	
8	320	54.6	509	1	OKHULK		protein-tyrosine kin	1.12e-34	
9	319	54.4	503	4	J01321		protein-tyrosine kin	1.64e-34	
10	319	54.4	509	4	A23639		protein-tyrosine kin	1.64e-34	
11	316	53.9	503	1	TVMSHC		protein-tyrosine kin	5.11e-34	
12	310	52.9	512	1	TVHULY		protein-tyrosine kin	4.95e-33	
13	310	52.9	526	1	TVFV60		protein-tyrosine kin	4.95e-33	
14	310	52.9	533	1	TVCHS		protein-tyrosine kin	4.95e-33	
15	310	52.9	557	1	TVFVS2		protein-tyrosine kin	4.95e-33	
16	310	52.9	568	1	TVFVS1		protein-tyrosine kin	4.95e-33	
17	310	52.9	587	1	TVFVPR		protein-tyrosine kin	4.95e-33	
18	308	52.6	541	4	A43610		protein-tyrosine kin	1.05e-32	
19	308	52.6	542	1	TVHUSC		protein-tyrosine kin	1.05e-32	

20	307	52.4	512	4	A39719	protein-tyrosine kin	1.54e-32
21	303	51.7	523	1	TVFVMT	protein-tyrosine kin	6.94e-32
22	303	51.7	534	4	S33568	protein-tyrosine kin	6.94e-32
23	303	51.7	537	1	TVHUSY	protein-tyrosine kin	6.94e-32
24	303	51.7	545	7	S52313	pp62v protein - Rous	6.94e-32
25	303	51.7	546	7	S52314	pp62v protein - Rous	6.94e-32
26	302	51.5	537	1	TVHUSR	protein-tyrosine kin	1.01e-31
27	300	51.2	534	4	A44991	protein-tyrosine kin	2.15e-31
28	299	51.0	537	4	A43806	protein-tyrosine kin	3.13e-31
29	299	51.0	541	12	S31645	protein-tyrosine kin	3.13e-31
30	299	51.0	663	1	TVMVRR	protein-tyrosine kin	3.13e-31
31	298	50.9	529	1	TVHUFR	protein-tyrosine kin	4.55e-31
32	297	50.7	536	4	S33569	protein-tyrosine kin	6.63e-31
33	297	50.7	537	4	A45501	protein-tyrosine kin	6.63e-31
34	297	50.7	543	1	TVHUYS	protein-tyrosine kin	6.63e-31
35	296	50.5	517	4	A43807	protein-tyrosine kin	9.66e-31
36	296	50.5	539	11	B49114	protein-tyrosine kin	9.66e-31
37	292	49.8	392	4	S04205	protein-tyrosine kin	4.33e-30
38	292	49.8	542	11	A49114	protein-tyrosine kin	4.33e-30
39	290	49.5	362	4	S24551	protein-tyrosine kin	9.16e-30
40	290	49.5	528	1	TVFVG9	protein-tyrosine kin	9.16e-30
41	290	49.5	541	1	TVCHYS	protein-tyrosine kin	9.16e-30
42	289	49.3	532	4	B34104	protein-tyrosine kin	1.33e-29
43	288	49.1	507	4	A39939	protein-tyrosine kin	1.94e-29
44	288	49.1	517	12	S24547	protein-tyrosine kin	1.94e-29
45	288	49.1	532	4	A34104	protein-tyrosine kin	1.94e-29

ALIGNMENTS

RESULT 1

ENTRY I38396 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human

ALTERNATE_NAMES FYN-related kinase (FRK)

ORGANISM #formal_name Homo sapiens #common_name man

DATE 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 15-Mar-1996

ACCESSIONS I38396

REFERENCE I38396

#authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.

#journal Gene (1994) 138:247-251

#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.

#cross-references MUID:94171047

#accession I38396

##status preliminary

##molecule_type mRNA

##residues 1-505 ##label RES

##cross-references EMBL:U00803; NID:g392887; CDS_PID:g392888

GENETICS

#gene GDB:FRK.

##cross-references GDB:G00-355-675

KEYWORDS phosphotransferase

SUMMARY #length 505 #molecular-weight 58254 #checksum 9379

Query Match 100.0X; Score 586; DB 11; Length 505;

Best Local Similarity 100.0X; Pred. No. 4.99e-80;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 wffgaigrsdaekqlllysenktgsflireseqkgefslsvldgavvkhyrikrldegff 175

Qy 122 WFFGAIGRSDAEKQLLYSENKTGSFLIRESEQKGEFSLSVLDGAVVKHYRIKRLDEGGF 181

Db 176 fltrrrrifstlnefvshytk 195

Qy 182 FLTRRRIFSTLNEFVSHYTK 201

RESULT 2

ENTRY A40092 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) blk - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Sep-1994

ACCESSIONS A40092

REFERENCE A40092

#authors Dynecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.

#journal Science (1990) 247:332-336

#title Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.

#cross-references MUID:90117147

#accession A40092

##status preliminary

##molecule_type mRNA

##residues 1-499 ##label DYM

##cross-references GB:M30903

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE

59-107 #domain SH3 homology #label SH3\

118-214 #domain SH2 homology #label SH2\

233-491 #domain protein kinase homology #label KIN\

241-249 #region protein kinase ATP-binding motif

SUMMARY #length 499 #molecular-weight 56644 #checksum 4536

Query Match 59.9%; Score 351; DB 4; Length 499;

Best Local Similarity 58.3%; Pred. No. 8.16e-40;

Matches 49; Conservative 17; Mismatches 14; Indels 4; Gaps 2;

Db 118 ufrtisrkd aerql lapankags flirese snkgafslsvkdittqgevvkhykirsld 177

||| :|:| :||:| | : ||:||||||| || ||||| : :| ||||:|: ||

Qy 122 WFFGAIGRSDAEKQLLYSENKTSFLIRESESQKGEFSLSV--L--DGAVVKHYRIKRLD 177

Db 178 nggyyisprifptlqalvqhysk 201

:||:::| |:|| :| ||:|

Qy 178 EGGFFLTRRRIFSTLNEFVSHYTK 201

RESULT 3

ENTRY TVHAST #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata

ORGANISM #formal_name Hydra attenuata

DATE 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1994

ACCESSIONS A34094

REFERENCE A34094

#authors Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.

#journal Mol. Cell. Biol. (1989) 9:4141-4151

#title Structure and expression of STK, a src-related gene in the simple metazoan Hydra attenuata.

#cross-references MUID:90066418

#accession A34094

##molecule_type mRNA

##residues 1-509 ##label BOS

##cross-references GB:M25245

GENETICS

#gene stk

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphoprotein; phosphotransferase; transforming protein; tyrosine-specific protein kinase

Query Match 45.9%; Score 51; DB 17; Length 3898;
Best Local Similarity 33.3%; Pred. No. 1.94e+02;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Search completed: Mon Feb 3 17:08:40 1997
Job time : 10 secs.

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

```
Run on:      Mon Feb  3 17:08:03 1997;  MasPar time 2.69 Seconds
           153.247 Million cell updates/sec
```

Tabular output not generated.

```
Title:          >US-08-426-509-4
Description:    (660-675) from US08426509.pep (5 of 5)
Perfect Score: 111
Sequence:      1 QQLSSIEPLREKDKH 16
```

Scoring table: PAN 150
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database:      pir48
               1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
               8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
               14:unrev
```

Statistics: Mean 27.034; Variance 49.322; scale 0.548

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	68	61.3	148	11	531791	stathmin - chicken	8.00e-01

2	68	61.3	149	5	A40936	stathmin - human	8.00e-01
3	68	61.3	149	12	B48917	stathmin - mouse	8.00e-01
4	68	61.3	149	5	A34294	stathmin - rat	8.00e-01
5	68	61.3	197	7	J01271	hypothetical 21.5K p	8.00e-01
6	65	58.6	1009	9	S61174	hypothetical protein	2.28e+00
7	62	55.9	678	10	S56284	hypothetical protein	6.30e+00
8	61	55.0	993	12	S49461	synaptonemal complex	8.79e+00
9	61	55.0	993	12	S59599	synaptonemal complex	8.79e+00
10	60	54.1	192	14	JC4573	Ras2 protein - Hydra	1.22e+01
11	60	54.1	192	10	S32042	RAS1 protein - Hydra	1.22e+01
12	59	53.2	805	1	YUPDS	sucrose synthase (EC	1.70e+01
13	58	52.3	243	8	S42873	probable succinate d	2.34e+01
14	58	52.3	605	3	ABPGS	serum albumin precur	2.34e+01
15	58	52.3	681	6	A36500	transferrin precurso	2.34e+01
16	58	52.3	2470	9	S57085	1-phosphatidylinosit	2.34e+01
17	57	51.4	437	11	S15704	transforming protein	3.22e+01
18	57	51.4	708	9	S53411	hypothetical protein	3.22e+01
19	57	51.4	763	6	S55616	glycoprotein H - equ	3.22e+01
20	56	50.5	179	12	A48917	SCG10 protein - mous	4.42e+01
21	56	50.5	179	5	A36110	SCG10 protein - rat	4.42e+01
22	56	50.5	237	7	JH0671	high-affinity branch	4.42e+01
23	56	50.5	239	7	JC4346	flagellar-specific s	4.42e+01
24	56	50.5	241	7	S47673	leucine transport pr	4.42e+01
25	56	50.5	494	1	B45738	alpha-amylase (EC 3.	4.42e+01
26	56	50.5	495	1	A45738	alpha-amylase (EC 3.	4.42e+01
27	56	50.5	508	9	S19697	aspartic proteinase	4.42e+01
28	56	50.5	598	3	RGE CNX	regulatory protein n	4.42e+01
29	56	50.5	660	12	A53618	regulatory protein N	4.42e+01
30	56	50.5	756	8	B64137	tetrahydropteroyltri	4.42e+01
31	56	50.5	808	4	S25526	sucrose synthase (EC	4.42e+01
32	56	50.5	808	4	S23543	sucrose synthase (EC	4.42e+01
33	56	50.5	985	10	A32240	REV1 protein - yeast	4.42e+01
34	56	50.5	1581	11	S49149	laninin A3 - human (4.42e+01
35	55	49.5	238	10	S22609	hypothetical protein	6.03e+01
36	55	49.5	373	7	S15200	hydrogenase isozyme	6.03e+01
37	55	49.5	406	8	S38218	hypothetical protein	6.03e+01
38	55	49.5	407	4	A49845	5-aminolevulinate sy	6.03e+01
39	55	49.5	607	3	ABBD5	serum albumin precur	6.03e+01
40	55	49.5	607	3	ABSHS	serum albumin precur	6.03e+01
41	55	49.5	807	4	S29242	sucrose synthase (EC	6.03e+01
42	54	48.6	406	12	S27010	aminoacylase (EC 3.5	8.21e+01
43	54	48.6	802	1	YU2MS	sucrose synthase (EC	8.21e+01
44	54	48.6	1025	4	JC1266	beta-galactosidase (8.21e+01
45	54	48.6	2016	10	S27411	cell division-associ	8.21e+01

ALIGNMENTS

```

RESULT      1
ENTRY       S31791      #type complete
TITLE       stathmin - chicken
ORGANISM    #formal_name Gallus gallus #common_name chicken
DATE        13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
            13-Jan-1995
ACCESSIONS  S31791
REFERENCE   S20720
#authors    Godbout, R.
#submission submitted to the EMBL Data Library, April 1992
#description Identification and characterization of transcripts present at
            elevated levels in the undifferentiated chick retina.
#accession  S31791
##status    preliminary
##molecule_type mRNA
##residues  1-148 ##label GOD
##cross-references EMBL:X67840
SUMMARY     #length 148 #molecular-weight 17082 #checksum 8231

```

Query Match 61.3%; Score 68; DB 11; Length 148;
Best Local Similarity 60.0%; Pred. No. 8.00e-01;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qmaaklerlrekdkh 129
|: : :| |||||
Qy 661 QLLSSIEPLREKDKH 675

RESULT 2

ENTRY A40936 #type complete
TITLE stathmin - human
ALTERNATE_NAMES leukemia-associated phosphoprotein p18; oncoprotein 18; Pr22
protein; proliferation-related phosphoprotein p18
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-May-1992 #sequence_revision 28-May-1992 #text_change
01-Mar-1996
ACCESSIONS A40936; A44780; S31624; S10565; A39215; S42211
REFERENCE A40936
#authors Melhem, R.F.; Zhu, X.; Hailat, N.; Strahler, J.R.; Hanash,
S.M.
#journal J. Biol. Chem. (1991) 266:17747-17753
#title Characterization of the gene for a proliferation-related
phosphoprotein (oncoprotein 18) expressed in high amounts
in acute leukemia.
#cross-references MUID:92011487
#accession A40936
##molecule_type DNA
##residues 1-149 ##label MEL
##cross-references GB:M31303
REFERENCE A44780
#authors Zhu, X.; Kozarsky, K.; Strahler, J.R.; Eckerskorn, C.;
Lottspeich, F.; Melhem, R.; Lowe, J.; Fox, D.A.; Hanash,
S.M.; Atweh, G.F.
#journal J. Biol. Chem. (1989) 264:14556-14560
#title Molecular cloning of a novel human leukemia-associated gene.
Evidence of conservation in animal species.
#accession A44780
##molecule_type mRNA
##residues 1-149 ##label ZHU
##cross-references GB:J04991
REFERENCE S31624
#authors Marunouchi, T.
#submission submitted to the EMBL Data Library, January 1992
#accession S31624
##status preliminary
##molecule_type mRNA
##residues 1-149 ##label MAR
##cross-references EMBL:Z11566
REFERENCE S10565
#authors Maucuer, A.; Doye, V.; Sobel, A.
#journal FEBS Lett. (1990) 264:275-278
#title A single amino acid difference distinguishes the human and
the rat sequences of stathmin, a ubiquitous intracellular
phosphoprotein associated with cell regulations.
#cross-references MUID:90292224
#accession S10565
##status preliminary
##molecule_type mRNA
##residues 1-149 ##label MAU
REFERENCE A39215
#authors Gullberg, M.; Noreus, K.; Brattsand, G.; Friedrich, B.;
Shingler, V.
#journal J. Biol. Chem. (1990) 265:17499-17505
#title Purification and characterization of a 19-kilodalton

intracellular protein. An activation-regulated putative
protein kinase C substrate of T lymphocytes.

#cross-references MUID:91009201

#accession A39215

##molecule_type protein

##residues 117-136 ##label GUL

REFERENCE S42211

#authors Brattsand, G.; Marklund, U.; Nylander, K.; Roos, G.;
Gullberg, M.

#journal Eur. J. Biochem. (1994) 220:359-368

#title Cell-cycle-regulated phosphorylation of oncoprotein 18 on
Ser16, Ser25 and Ser38.

#accession S42211

##status preliminary

##molecule_type protein

##residues 11-44 ##label BRA

GENETICS

#gene GDB:LAP18

##cross-references GDB:G00-127-971

#map_position 1p36.1-p35

CLASSIFICATION #superfamily stathmin

KEYWORDS cytosol; phosphoprotein

FEATURE

16,25,38 #binding_site phosphate (Ser) (covalent) #status
experimental

SUMMARY #length 149 #molecular-weight 17302 #checksum 1901

Query Match 61.3%; Score 68; DB 5; Length 149;

Best Local Similarity 60.0%; Pred. No. 8.00e-01;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qnaaklerlrekdkh 129

|: : :| |||||

Qy 661 QLLSSIEPLREKDKH 675

RESULT 3

ENTRY B48917 #type complete

TITLE stathmin - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change
01-Dec-1995

ACCESSIONS B48917

REFERENCE A48917

#authors Okazaki, T.; Yoshida, B.N.; Avraham, K.B.; Wang, H.;
Wuenschell, C.W.; Jenkins, N.A.; Copeland, N.G.; Anderson,
D.J.; Mori, N.

#journal Genomics (1993) 18:360-373

#title Molecular diversity of the SCG10/stathmin gene family in the
mouse.

#accession B48917

##status preliminary

##molecule_type DNA

##residues 1-149 ##label OKA

##cross-references GB:L20258

##note authors translated the codon GAT for residue 34 as Glu

SUMMARY #length 149 #molecular-weight 17274 #checksum 2075

Query Match 61.3%; Score 68; DB 12; Length 149;

Best Local Similarity 60.0%; Pred. No. 8.00e-01;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qnaaklerlrekdkh 129

|: : :| |||||

Qy 661 QLLSSIEPLREKDKH 675

RESULT 4

ENTRY A34294 #type complete

TITLE stathmin - rat

ALTERNATE_NAMES phosphoprotein p19

ORGANISM #formal_name Rattus norvegicus #common_name Norway rat

DATE 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993

ACCESSIONS A34294; A32892

REFERENCE A34294

#authors Doye, V.; Soubrier, F.; Bauw, G.; Bouterin, M.C.; Beretta, L.; Koppel, J.; Vandekerckhove, J.; Sobel, A.

#journal J. Biol. Chem. (1989) 264:12134-12137

#title A single cDNA encodes two isoforms of stathmin, a developmentally regulated neuron-enriched phosphoprotein.

#cross-references MUID:89308626

#accession A34294

##molecule_type mRNA

##residues 1-149 ##label DOY

##cross-references GB:J04979

REFERENCE A32892

#authors Schubart, U.K.; Banerjee, M.D.; Eng, J.

#journal DNA (1989) 8:389-398

#title Homology between the cDNAs encoding phosphoprotein p19 and SCG10 reveals a novel mammalian gene family preferentially expressed in developing brain.

#cross-references MUID:89377477

#accession A32892

##molecule_type mRNA

##residues 1-149 ##label SCH

##cross-references GB:M27876

CLASSIFICATION #superfamily stathmin

SUMMARY #length 149 #molecular-weight 17288 #checksum 2109

Query Match 61.3%; Score 68; DB 5; Length 149;

Best Local Similarity 60.0%; Pred. No. 8.00e-01;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qnaaklerlrekdkh 129

| : : | |||||

Qy 661 QLLSSIEPLREKDKH 675

RESULT 5

ENTRY J01271 #type complete

TITLE hypothetical 21.5K protein - Escherichia coli

ALTERNATE_NAMES ORFE protein

ORGANISM #formal_name Escherichia coli

DATE 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 27-Jan-1995

ACCESSIONS J01271; S24198

REFERENCE J01271

#authors Wachi, M.; Doi, M.; Ueda, T.; Ueki, M.; Tsuritani, K.; Nagai, K.; Matsuhashi, M.

#journal Gene (1991) 106:135-136

#title Sequence of the downstream flanking region of the shape-determining genes mreBCD of Escherichia coli.

#cross-references MUID:92039056

#accession J01271

##molecule_type DNA

##residues 1-197 ##label WAC

##cross-references EMBL:X57166

COMMENT The gene encoding for this protein is located at downstream of the mre genes.

SUMMARY #length 197 #molecular-weight 21515 #checksum 3123

Result	Z				Query						
No.	Score	Match	Length	DB	ID	Description	Pred.	No.			
1	1327	71.9	659	11	I37212	Bruton agammaglobuli	2.40e-218				
2	1327	71.9	659	11	S28912	protein-tyrosine kin	2.40e-218				
3	1299	70.4	660	12	JN0471	protein-tyrosine kin	4.41e-213				
4	1288	69.8	659	12	B45184	B cell progenitor ki	5.15e-211				
5	1255	68.0	527	12	A55631	protein-tyrosine kin	8.12e-205				
6	1223	66.3	527	4	S13763	protein-tyrosine kin	8.20e-199				
7	1207	65.4	608	4	JU0227	protein-tyrosine kin	8.20e-196				
8	1207	65.4	630	4	JU0228	protein tyrosine kin	8.20e-196				
9	1188	64.4	602	4	JU0215	tyrosine kinase, tec	2.98e-192				
10	1168	63.3	620	4	S33253	protein-tyrosine kin	1.66e-188				
11	1157	62.7	619	4	A47333	T-cell-specific tyro	1.91e-186				
12	1157	62.7	625	4	A43030	protein-tyrosine kin	1.91e-186				
13	1129	61.2	619	4	JN0472	protein-tyrosine kin	3.30e-181				
14	1117	60.5	590	1	TVFFDS	protein-tyrosine kin	5.79e-179				
15	915	49.6	506	4	S24553	protein-tyrosine kin	2.35e-141				
16	860	46.6	362	4	S24551	protein-tyrosine kin	3.54e-131				
17	858	46.5	1520	1	TVFFA	protein-tyrosine kin	8.29e-131				
18	847	45.9	507	4	A39939	protein-tyrosine kin	8.92e-129				
19	844	45.7	505	4	S24550	protein-tyrosine kin	3.19e-128				
20	836	45.3	509	4	A23639	protein-tyrosine kin	9.56e-127				
21	835	45.3	509	1	OKHULK	protein-tyrosine kin	1.46e-126				
22	826	44.8	509	1	TVHAST	protein-tyrosine kin	6.68e-125				
23	824	44.7	308	1	TVFFS	protein-tyrosine kin	1.56e-124				

24	823	44.6	542	11	A49114	protein-tyrosine kin	2.39e-124
25	821	44.5	557	10	A00629	protein-tyrosine kin	5.58e-124
26	819	44.4	334	4	S24552	protein-tyrosine kin	1.30e-123
27	820	44.4	697	7	A26132	gag-abl-pol polyprot	8.53e-124
28	817	44.3	1130	1	TVHUA	protein-tyrosine kin	3.05e-123
29	815	44.2	537	4	A43806	protein-tyrosine kin	7.12e-123
30	815	44.2	981	1	F0MVGM	gag-abl polyprotein	7.12e-123
31	815	44.2	1123	4	A39962	kinase-related trans	7.12e-123
32	812	44.0	537	1	TVHUSY	protein-tyrosine kin	2.54e-122
33	809	43.8	505	11	S51647	protein-tyrosine kin	9.07e-122
34	808	43.8	537	1	TVHUSR	protein-tyrosine kin	1.39e-121
35	802	43.5	539	11	B49114	protein-tyrosine kin	1.76e-120
36	800	43.4	536	4	S33569	protein-tyrosine kin	4.12e-120
37	798	43.3	568	1	TVFVS1	protein-tyrosine kin	9.61e-120
38	799	43.3	1146	4	B35962	protein-tyrosine kin	6.29e-120
39	799	43.3	1182	4	A35962	protein-tyrosine kin	6.29e-120
40	797	43.2	526	1	TVFV60	protein-tyrosine kin	1.47e-119
41	797	43.2	532	4	A34104	protein-tyrosine kin	1.47e-119
42	797	43.2	532	4	B34104	protein-tyrosine kin	1.47e-119
43	796	43.1	505	11	I38396	protein-tyrosine kin	2.24e-119
44	796	43.1	541	4	A43610	protein-tyrosine kin	2.24e-119
45	796	43.1	542	1	TVHUSC	protein-tyrosine kin	2.24e-119

ALIGNMENTS

RESULT 1

ENTRY I37212 #type complete

TITLE Bruton agammaglobulinemia tyrosine kinase - human

ORGANISM #formal_name Homo sapiens #common_name man

DATE 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 09-Mar-1996

ACCESSIONS I37212

REFERENCE I37212

#authors Ohta, Y.; Haire, R.N.; Litman, R.T.; Fu, S.M.; Nelson, R.P.; Kratz, J.; Kornfeld, S.J.; de la Morena, M.; Good, R.A.; Litman, G.W.

#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9062-9066

#title Genomic organization and structure of Bruton agammaglobulinemia tyrosine kinase: localization of mutations associated with varied clinical presentations and course in X chromosome-linked agammaglobulinemia.

#cross-references NUID:94377492

#accession I37212

##status preliminary

##molecule_type DNA

##residues 1-659 ##label RES

##cross-references EMBL:U10087; NID:g517436; CDS_PID:g517438

##note only intron-exon junctions are shown

GENETICS

#gene GDB:BTK; AGMX1; IND1

##cross-references GDB:G00-120-542

#map_position Xq21.33-q22

#introns 47/3; 80/3; 103/3; 131/1; 174/1; 196/3; 259/2; 280/2; 298/3; 325/2; 368/1; 393/1; 450/2; 522/3; 544/2; 584/1; 636/3

SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 71.9%; Score 1327; DB 11; Length 659;

Best Local Similarity 67.8%; Pred. No. 2.40e-218;

Matches 160; Conservative 41; Mismatches 35; Indels 0; Gaps 0;

Db 409 gtgqfgvvkygkurgqydvai knikegmsedefieeakvmmnlshelkvlygvctkqr 468

|:||||| |:|:|||||:|||||:|||||:| | |:| | | | |:| | | |

Gy 424 GSG@FGVV@LGKWK@YDVAVKMIKEGMSDEFF@EA@TMMKLSHPKLVKFYGVCSKEY 483

Db 469 pifiiteumangcllnulremhrfqtqallencdkvceaneuleskqflhrdlaarnc1 528

```
ENTRY      JN0471      #type complete
TITLE      protein-tyrosine kinase (EC 2.7.1.112) emb - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
            12-May-1995
```



```

ACCESSIONS      JN0471
REFERENCE       JN0471
#authors        Yanada, N.; Kawakami, Y.; Kimura, H.; Fukunachi, H.; Baier,
                G.; Altman, A.; Kato, T.; Inagaki, Y.; Kawakami, T.
#journal        Biochem. Biophys. Res. Commun. (1993) 192:231-240
#title          Structure and expression of novel protein-tyrosine kinases,
                Erb and ErbB, in the hematopoietic cells.
#accession      JN0471
##molecule_type mRNA
##residues      1-660 ##label YAM
##note          the nucleotide sequence is not given

```

```
Dbb    409 gtgqfgvvk ygkgurggydvai kmiregsmsedefieeakvnmnlsheklvlqlygvctkqr   468  
      |:||||| ||::|||:::||:|||||||:::|| ||:|| | :|||:|:  
@y     424 GSGQFGVVQLGKWKGGYDVAVKMIKEGSMSDEFFQEAGTMMKL SHPKLVKFYGVC SKEY   483
```

```
Dbb    469 pifiiteymangcllnylremrhrfqtqllemckdvc eameyles kqflhr dlaarnc l   528  
      |:|:||||::||| ||| :: ||||| ||||:| :|| ||:|||||||  
@y     484 PIYIVTEYISNGCLLNYLRSHKGLEPSQLLEN CYDVCEGM AFLESHOFIHRDLAARN CL   543
```

```
Dbb    529 vndqqgvkvslpglrsyvlddeytssvg skfpvrwsppevlayskf ssksdia wafgvlmw   588  
      |: : ||| |:|||||:| |||:||||:|:|:|:| |:||||:||||:|  
@y     544 VDRDLCVKSVD FGMTRYVLDDGYVS SVGT KFP VKWSAPEVFHYFKYS SKSD VWAFGI LMW   603
```

```
Dbb    589 eiyslgkp pyerft nsetae hia qgrlrph laservyti ngscwh ekaderps f   644  
      |:|||| ||: : ||: :|| |||||||: :| ||||||| : : ||:|  
@y     604 EVFSLGKPYPDYDNSOVVLKVSGHRLRPHLASDT IYQIM YSCWHELPEKRPT F   659
```

```

RESULT      5
ENTRY       A55631      #type complete
TITLE       protein-tyrosine kinase (EC 2.7.1.112) rtk - mouse
ALTERNATE_NAMES  resting lymphocyte kinase
ORGANISM     #formal_name Mus sp. #common_name mouse
DATE         23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
              12-May-1995
ACCESSIONS   A55631
REFERENCE     A55631
              #authors   Hu, Q.; Davidson, D.; Schwartzberg, P.L.; Macchiarini, F.;
              Lenardo, M.J.; Bluestone, J.A.; Matis, L.A.
              #journal    J. Biol. Chem. (1995) 270:1928-1934
              #title      Identification of rtk, a novel protein tyrosine kinase with
              predominant expression in the T cell lineage.
              #accession   A55631
                  ##status      preliminary
                  ##molecule_type mRNA
                  ##residues     1-527 ##label HUA
                  ##cross-references GB:L35268
CLASSIFICATION #superfamily SH3 homology; protein kinase homology
KEYWORDS       phosphotransferase
FEATURE
      89-137      #domain SH3 homology #label SH3\
      269-527     #domain protein kinase homology #label KIN
SUMMARY        #length 527 #molecular-weight 61108 #checksum 785

Query Match      68.0%;  Score 1255;  DB 12;  Length 527;
Best Local Similarity 65.5%;  Pred. No. 8.12e-205;
Matches 156;  Conservative 40;  Mismatches 38;  Indels 4;  Gaps 4

```

```
Db      278 gsgqfgvyhlgeurahipvaikainegsnseedfieakvnaqlshslvlqlygvciqqk 337  
        |||||::|| ::: ||: |:|||||:::|| |:::::| :||| :  
Qu     424 GSGQFGVVQLGKWKQGYDVAVKKIKESMSDEFFQEAQTMMKLSPKLVKFYGVCSKEY 483
```

Db 338 plviivtefmcngclldylrer-kgqlqkalllsacqdicgmaylerscihrdlaarnc 396
 |:|||||: | |||:| | : | | : | | | | :|||||:| | :|||||
 Qy 484 PIYIVTEYISNGCLLNYLRSHGKG-LEPSQLENCYDVCEGMAFLESHQFIHRDLAARNC 542

Db 397 lvssa-cvvkisdfignaryvlddeyisssgakfpvkwcpevfhnkyssksdvwsfgvl 455
 | | | | :|||||:|||||:| | | | :||||| :||||| :|||||:| |:
 Qy 543 LVDRDLCV-KVSDFGMTRYVLDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGIL 601

Db 456 mwevftegapfenksnlqvveaisqgfrlyrphlapntiyrvmyscwhepskgrptf 513
 |||||: | | : : | || | :|| | |||||: |||:||||| | ||||
 Qy 602 MWEVSLGKQPYDLYDNSQVVLKVSQGHRLYRPHLASDTIYQIMYSCWHELPEKRPTF 659

RESULT 6

ENTRY S13763 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) tec - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
 08-Dec-1995

ACCESSIONS S13763
 REFERENCE S13763
 #authors Mano, H.; Ishikawa, F.; Nishida, J.; Hirai, H.; Takaku, F.
 #journal Oncogene (1990) 5:1781-1786
 #title A novel protein-tyrosine kinase, tec, is preferentially
 expressed in liver.
 #cross-references MUID:91133729
 #accession S13763
 ##molecule_type mRNA
 ##residues 1-527 ##label MAN
 ##cross-references EMBL:X55663

GENETICS
 #gene tec

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase
 homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE
 104-142 #domain SH3 homology #status atypical #label SH3\
 264-522 #domain protein kinase homology #label KIN

SUMMARY #length 527 #molecular-weight 61556 #checksum 5620

Query Match 66.3%; Score 1223; DB 4; Length 527;
 Best Local Similarity 61.0%; Pred. No. 8.20e-199;
 Matches 144; Conservative 45; Mismatches 47; Indels 0; Gaps 0;

Db 273 gsglfgvvrllgkuraqykvaikaireganceedfieakvnmklthpklvqlygvctqqk 332
 ||| ||||:||||:| | | | :||| | :||:| | ||||:|||| | ||||: |
 Qy 424 GSGQFGVVQLGKWKQGYDVAVKMIKEGSMSEDEFFQEAQTMMKLSHPKLVKFYGVCSKEY 483

Db 333 piyivtefmergcllnflrqrqghfsrdmllsncqdvcegmeylernsfihrdlaarncl 392
 |||||: | |||:| | : | | | | ||||| :| | : |||||
 Qy 484 PIYIVTEYISNGCLLNYLRSHGKGLEPSQLENCYDVCEGMAFLESHQFIHRDLAARNCL 543

Db 393 vneagvvkvsdfgmaryvlddqytsssgakfpvkwcpevfnyrsfsksksdvwsfgvlmw 452
 | : | |||||:||||| | | | :||||| :||||| :|||||:| |:
 Qy 544 VDRDLCVKVSDFGMTRYVLDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGILMW 603

Db 453 eiftegrapfekntngevvtavtrghrlhrpklatkylgevmrlcwqerpegrpsf 508
 | : | : | : | : | | :| | :| :| | | | :| :| | | | | | :|
 Qy 604 EVFSLGKQPYDLYDNSQVVLKVSQGHRLYRPHLASDTIYQIMYSCWHELPEKRPTF 659

RESULT 7

ENTRY JU0227 #type complete
 TITLE protein-tyrosine kinase (EC 2.7.1.112) tec III - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 31-Dec-1993 #sequence revision 31-Dec-1993 #text change